STIC Search Report
Biotech-Chem Library

STIC Database Tracking Number: 131974

TO: James Schultz
Location: rem/2d18/2c18
Art Unit: 1635
Wednesday, September 15, 2004
Case Serial Number: 10/019470

From: Paul Schulwitz
Location: Biotech-Chem Library
REM-1A65
Phone: (571)272-2527

paul.schulwitz@uspto.gov

Search Notes

Examiner Schultz,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

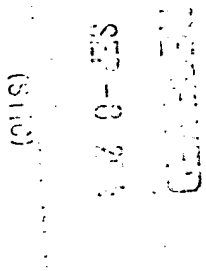
Paul Schulwitz
Technical Information Specialist
STIC Biotech/Chem Library
(571)272-2527

STIC-Biotech/ChemLib 131974 mep

From: Schultz, James
Sent: Wednesday, September 08, 2004 1:27 PM
To: STIC-Biotech/ChemLib
Subject: Seq Search 10/019,470

Hello,
Could you please run a length limited nucleotide sequence search on SEQ ID NO: 1 in the above entitled case which returns hits 30 nucleotides long and under?
Thanks,
Doug Schultz

James Douglas Schultz, PhD
AU 1635 (Biotechnology)
Patent Examiner
United States Patent and Trademark Office
(Office) REM 2D18
(Mail) REM 2C18
(571) 272-0763



****
STAFF USE ONLY

Searcher:_____
Searcher Phone: 2-
Date Searcher Picked up:____
Date Completed: 9/15
Searcher Prep/Rev. Time:___
Online Time:_____

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Type of Search
NA Sequence: #_____
AA Sequence :#_____
Structure: #_____
Bibliographic:_____
Litigation:_____
Patent Family:_____
Other:_____

****
Vendors and cost where applicable
STN:_____
DIALOG:_____
QUESTEL/ORBIT:_____
LEXIS/NEXIS:_____
SEQUENCE SYSTEM:_____
WWW/Internet:_____
Other(Specify):_____

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: September 15, 2004, 03:47:35 ; Search time 10899 Seconds
(without alignments)
11246.362 Million cell updates/sec

Title: US-10-019-470-1
Perfect score: 2828
Sequence: 1 gttgaaagctcctggcgcgg.....aaagtgtcaatttccaagga 2828

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 1237800

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
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8: gb_pl:*
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11: gb_sts:*
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15: em_ba:*
16: em_fun:*
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30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		20.6	0.7	21	6	AX096602	AX096602 Sequence
2		20.6	0.7	21	6	AX096603	AX096603 Sequence
3		20.6	0.7	21	6	AX096604	AX096604 Sequence
4		20.6	0.7	21	6	AX096605	AX096605 Sequence
5		20.6	0.7	21	6	AX096606	AX096606 Sequence
6		20.6	0.7	21	6	AX153968	AX153968 Sequence
7		20.6	0.7	21	6	AX153969	AX153969 Sequence
8		20.6	0.7	21	6	AX153970	AX153970 Sequence
9		20.6	0.7	21	6	AX153971	AX153971 Sequence
10		20.6	0.7	21	6	AX153972	AX153972 Sequence
11		20.6	0.7	21	6	AX153973	AX153973 Sequence
12		20.6	0.7	21	6	AX153974	AX153974 Sequence
13		20	0.7	30	6	AX791874	AX791874 Sequence
14	c	19.6	0.7	27	6	AX458310	AX458310 Sequence
15	c	19.6	0.7	27	6	BD187418	BD187418 Novel pol
16		19.6	0.7	30	6	A17675	A17675 Nucleotide
17		19.6	0.7	30	6	AR016317	AR016317 Sequence
18		19	0.7	29	6	AX306690	AX306690 Sequence
19	c	18.8	0.7	24	6	AX292738	AX292738 Sequence
20	c	18.2	0.6	24	6	BD268732	BD268732 Inhibitor
21	c	18.2	0.6	24	6	AR229129	AR229129 Sequence
22	c	18.2	0.6	24	6	AR281392	AR281392 Sequence
23	c	18.2	0.6	24	6	AR304601	AR304601 Sequence
24	c	18.2	0.6	24	6	AR337597	AR337597 Sequence
25		18.2	0.6	27	6	AR287463	AR287463 Sequence
26		18.2	0.6	28	6	AR282887	AR282887 Sequence
27		18.2	0.6	28	6	AX052812	AX052812 Sequence
28	c	18	0.6	30	6	A98653	A98653 Sequence 9
29	c	17.8	0.6	21	6	AR067354	AR067354 Sequence
30		17.8	0.6	21	6	AX094946	AX094946 Sequence
31	c	17.8	0.6	25	6	AR078206	AR078206 Sequence
32	c	17.8	0.6	25	6	AR081978	AR081978 Sequence
33	c	17.8	0.6	25	6	AR139684	AR139684 Sequence
34	c	17.8	0.6	25	6	BD140131	BD140131 Diagnosis
35	c	17.8	0.6	27	6	A56639	A56639 Sequence 6
36	c	17.8	0.6	27	6	A80360	A80360 Sequence 6
37	c	17.8	0.6	27	6	AR111763	AR111763 Sequence
38	c	17.8	0.6	28	6	AR137966	AR137966 Sequence
39	c	17.8	0.6	28	6	BD265691	BD265691 Transcrip
40	c	17.8	0.6	30	6	AX577834	AX577834 Sequence
41		17.8	0.6	30	6	AX793968	AX793968 Sequence
42	c	17.6	0.6	24	6	AX299470	AX299470 Sequence
43		17.6	0.6	27	6	AX711384	AX711384 Sequence
44		17.6	0.6	30	6	A17666	A17666 Nucleotide
45		17.6	0.6	30	6	AR016319	AR016319 Sequence

ALIGNMENTS

RESULT 1
AX096602
LOCUS AX096602 21 bp DNA linear PAT 30-MAR-2001
DEFINITION Sequence 1780 from Patent WO0118250.
ACCESSION AX096602
VERSION AX096602.1 GI:13512856
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Lander,E.S., Gargill,M., Ireland,J.S., Bolk,S., Daley,G.Q. and
Mccarthy,J.J.
TITLE Single nucleotide polymorphisms in genes

```
  JOURNAL   Patent: WO 0118250-A 1780 15-MAR-2001;
            WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Millennium
            Pharmaceuticals, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Homo sapiens"
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ORIGIN

  Query Match             0.7%;  Score 20.6;  DB 6;  Length 21;
  Best Local Similarity   95.2%;  Pred. No. 9.1e+06;
  Matches   20;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1123 AGCTGAATGATACTCACCCTC 1143
              ||||||||||:|||||||||||
Db          1 AGCTGAATGAYACTCACCCTC 21


RESULT 2
AX096603
LOCUS       AX096603                 21 bp    DNA     linear   PAT 30-MAR-2001
DEFINITION  Sequence 1781 from Patent WO0118250.
ACCESSION   AX096603
VERSION     AX096603.1  GI:13512857
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Lander,E.S., Gargill,M., Ireland,J.S., Bolk,S., Daley,G.Q. and
            Mccarthy,J.J.
  TITLE     Single nucleotide polymorphisms in genes
  JOURNAL   Patent: WO 0118250-A 1781 15-MAR-2001;
            WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Millennium
            Pharmaceuticals, Inc. (US)
FEATURES             Location/Qualifiers
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

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Qy       1978 AGCTGATCACTTCAGTGGCAG 1998
              ||||||||||:|||||||||||
Db          1 AGCTGATCACYTCAGTGGCAG 21


RESULT 3
AX096604
LOCUS       AX096604                 21 bp    DNA     linear   PAT 30-MAR-2001
DEFINITION  Sequence 1782 from Patent WO0118250.
ACCESSION   AX096604
VERSION     AX096604.1  GI:13512858
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Lander,E.S., Gargill,M., Ireland,J.S., Bolk,S., Daley,G.Q. and
            Mccarthy,J.J.
  TITLE     Single nucleotide polymorphisms in genes
  JOURNAL   Patent: WO 0118250-A 1782 15-MAR-2001;
            WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Millennium
            Pharmaceuticals, Inc. (US)
FEATURES             Location/Qualifiers
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

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  Matches   20;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1873 TGTACAACCGCATTAAGAAAG 1893
              ||||||||||:|||||||||||
Db          1 TGTACAACCGYATTAAGAAAG 21


RESULT 4
AX096605
LOCUS       AX096605                 21 bp    DNA     linear   PAT 30-MAR-2001
DEFINITION  Sequence 1783 from Patent WO0118250.
ACCESSION   AX096605
VERSION     AX096605.1  GI:13512859
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Lander,E.S., Gargill,M., Ireland,J.S., Bolk,S., Daley,G.Q. and
            Mccarthy,J.J.
  TITLE     Single nucleotide polymorphisms in genes
  JOURNAL   Patent: WO 0118250-A 1783 15-MAR-2001;
            WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Millennium
            Pharmaceuticals, Inc. (US)
FEATURES             Location/Qualifiers
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ORIGIN

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Qy       2027 AAGCAAGTTGAAAGTCATCTT 2047
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Db          1 AAGCAAGTTGRAAGTCATCTT 21


RESULT 5
AX096606
LOCUS       AX096606                 21 bp    DNA     linear   PAT 30-MAR-2001
DEFINITION  Sequence 1784 from Patent WO0118250.
ACCESSION   AX096606
VERSION     AX096606.1  GI:13512860
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Lander,E.S., Gargill,M., Ireland,J.S., Bolk,S., Daley,G.Q. and
            Mccarthy,J.J.
  TITLE     Single nucleotide polymorphisms in genes
  JOURNAL   Patent: WO 0118250-A 1784 15-MAR-2001;
            WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Millennium
            Pharmaceuticals, Inc. (US)
FEATURES             Location/Qualifiers
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN
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Qy       1377 GATGTGGACCCTCTGAGAAGG 1397
              ||||||||||:||||||||||
Db          1 GATGTGGACCSTCTGAGAAGG 21


RESULT 6
AX153968
LOCUS       AX153968                  21 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 66 from Patent WO0138576.
ACCESSION   AX153968
VERSION     AX153968.1  GI:14535582
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Cargill,M., Ireland,J.S. and Lander,E.S.
  TITLE     Human single nucleotide polymorphisms
  JOURNAL   Patent: WO 0138576-A 66 31-MAY-2001;
            WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)
FEATURES             Location/Qualifiers
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                     /mol_type="unassigned DNA"
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ORIGIN

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  Matches   20;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1218 AACCAGAAGACCTTCGCCTAC 1238
              ||||||||||:||||||||||
Db          1 AACCAGAAGASCTTCGCCTAC 21


RESULT 7
AX153969
LOCUS       AX153969                  21 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 67 from Patent WO0138576.
ACCESSION   AX153969
VERSION     AX153969.1  GI:14535583
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Cargill,M., Ireland,J.S. and Lander,E.S.
  TITLE     Human single nucleotide polymorphisms
  JOURNAL   Patent: WO 0138576-A 67 31-MAY-2001;
            WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)
FEATURES             Location/Qualifiers
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Qy       1706 CCTCCGGGAACTCGCCAAGGT 1726
              ||||||||||:||||||||||
Db          1 CCTCCGGGAAMTCGCCAAGGT 21


RESULT 8
AX153970
LOCUS       AX153970                  21 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 68 from Patent WO0138576.
ACCESSION   AX153970
VERSION     AX153970.1  GI:14535584
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Cargill,M., Ireland,J.S. and Lander,E.S.
  TITLE     Human single nucleotide polymorphisms
  JOURNAL   Patent: WO 0138576-A 68 31-MAY-2001;
            WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)
FEATURES             Location/Qualifiers
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Qy       2003 GGTGAACAATGACCCTATGGT 2023
              ||||||||||:||||||||||
Db          1 GGTGAACAATRACCCTATGGT 21


RESULT 9
AX153971
LOCUS       AX153971                  21 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 69 from Patent WO0138576.
ACCESSION   AX153971
VERSION     AX153971.1  GI:14535585
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Cargill,M., Ireland,J.S. and Lander,E.S.
  TITLE     Human single nucleotide polymorphisms
  JOURNAL   Patent: WO 0138576-A 69 31-MAY-2001;
            WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)
FEATURES             Location/Qualifiers
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Qy       2119 CTGCAGGCACCGAAGCCTCGG 2139
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Db          1 CTGCAGGCACYGAAGCCTCGG 21


RESULT 10
AX153972
LOCUS       AX153972                  21 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 70 from Patent WO0138576.
ACCESSION   AX153972
VERSION     AX153972.1  GI:14535586
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
  AUTHORS  Cargill,M., Ireland,J.S. and Lander,E.S.
  TITLE    Human single nucleotide polymorphisms
  JOURNAL  Patent: WO 0138576-A 70 31-MAY-2001;
           WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)
FEATURES             Location/Qualifiers
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ORIGIN

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Db          1 TGGCTGCTTTRGACAAGAAAG 21


RESULT 11
AX153973
LOCUS       AX153973                 21 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 71 from Patent WO0138576.
ACCESSION   AX153973
VERSION     AX153973.1  GI:14535587
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
  AUTHORS  Cargill,M., Ireland,J.S. and Lander,E.S.
  TITLE    Human single nucleotide polymorphisms
  JOURNAL  Patent: WO 0138576-A 71 31-MAY-2001;
           WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)
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ORIGIN

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RESULT 12
AX153974
LOCUS       AX153974                 21 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 72 from Patent WO0138576.
ACCESSION   AX153974
VERSION     AX153974.1  GI:14535588
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
  AUTHORS  Cargill,M., Ireland,J.S. and Lander,E.S.
  TITLE    Human single nucleotide polymorphisms
  JOURNAL  Patent: WO 0138576-A 72 31-MAY-2001;
           WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)
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Qy       2350 TTGACAATGGCTTTTTTTCTC 2370
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Db          1 TTGACAATGGYTTTTTTTCTC 21


RESULT 13
AX791874
LOCUS       AX791874                 30 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Sequence 4338 from Patent WO02066501.
ACCESSION   AX791874
VERSION     AX791874.1  GI:32957321
KEYWORDS    .
SOURCE      Helicobacter pylori
  ORGANISM  Helicobacter pylori
           Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
           Helicobacteraceae; Helicobacter.
REFERENCE  1
  AUTHORS  Legrain,P., Rain,J.C., Colland,F., de Reuse,H. and Labigne,A.
  TITLE    Protein-protein interactions in Helicobacter pylori
  JOURNAL  Patent: WO 02066501-A 4338 29-AUG-2002;
           Hybrigenics (FR) ; INSTITUT PASTEUR (FR)
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="Helicobacter pylori"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:210"
ORIGIN

  Query Match             0.7%;  Score 20;  DB 6;  Length 30;
  Best Local Similarity   82.1%;  Pred. No. 1.3e+07;
  Matches   23;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2397 ATCATCAACATGCTATTTTATCATGACA 2424
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Db          2 ATCATCATCATGGTATTTTTTCATAAGA 29


RESULT 14
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LOCUS       AX458310                 27 bp    DNA     linear   PAT 08-JUL-2002
DEFINITION  Sequence 5 from Patent EP1215214.
ACCESSION   AX458310
VERSION     AX458310.1  GI:21725003
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
  AUTHORS  Fidock,M.D.
  TITLE    Novel polypeptide
  JOURNAL  Patent: EP 1215214-A 5 19-JUN-2002;
           Pfizer Limited (GB) ; PFIZER INC. (US)
FEATURES             Location/Qualifiers
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ORIGIN

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  Best Local Similarity   84.6%;  Pred. No. 1.5e+07;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;
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Qy       1415 GGAAGGAAGCAAAAGGATCAACATGG 1440
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Db         27 GGAAGGAAGCAAAATGGACAGCATGG 2


RESULT 15
BD187418/c
LOCUS       BD187418                  27 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Novel polypeptide.
ACCESSION   BD187418
VERSION     BD187418.1  GI:32997157
KEYWORDS    JP 2003009885-A/3.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Fidock,M.D.
  TITLE     Novel polypeptide
  JOURNAL   Patent: JP 2003009885-A 3 14-JAN-2003;
            Pfizer Ltd (EP(GB) only),Pfizer Inc (US JP EP except GB)
COMMENT     OS   Homo sapiens
            PN   JP 2003009885-A/3
            PD   14-JAN-2003
            PF   17-DEC-2001 JP 2001382707
            PR   18-DEC-2000 GB    0030855.1,17-JAN-2001 GB    0101222.8 PI
            mark david fidock
            CC
            FH   Key             Location/Qualifiers.
FEATURES                Location/Qualifiers
     source             1. .27
                        /organism="Homo sapiens"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:9606"
ORIGIN

  Query Match             0.7%;  Score 19.6;  DB 6;  Length 27;
  Best Local Similarity   84.6%;  Pred. No. 1.5e+07;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1415 GGAAGGAAGCAAAAGGATCAACATGG 1440
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Db         27 GGAAGGAAGCAAAATGGACAGCATGG 2


Search completed: September 15, 2004, 10:39:44
Job time : 10903 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: September 14, 2004, 23:41:54 ; Search time 1053 Seconds
(without alignments)
11409.216 Million cell updates/sec

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Perfect score: 2828
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 2723956

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	27	1.0	27	3	AAA14004	Aaa14004 Human liv
c	2	21	0.7	21	3	AAA14003	Aaa14003 Human liv
	3	21	0.7	21	3	AAA14002	Aaa14002 Human liv
	4	21	0.7	21	4	AAF97019	Aaf97019 Human gen
	5	21	0.7	21	4	AAF97017	Aaf97017 Human gen
	6	21	0.7	21	4	AAF97016	Aaf97016 Human gen
	7	21	0.7	21	4	AAF97015	Aaf97015 Human gen
	8	21	0.7	21	4	AAF97018	Aaf97018 Human gen
	9	21	0.7	21	4	AAH62165	Aah62165 Phosphory
	10	21	0.7	21	4	AAH62170	Aah62170 Phosphory
	11	21	0.7	21	4	AAH62169	Aah62169 Phosphory
	12	21	0.7	21	4	AAH62167	Aah62167 Phosphory
	13	21	0.7	21	4	AAH62171	Aah62171 Phosphory
	14	21	0.7	21	4	AAH62166	Aah62166 Phosphory
	15	21	0.7	21	4	AAH62168	Aah62168 Phosphory
c	16	20	0.7	20	3	AAA14030	Aaa14030 Human liv
c	17	20	0.7	20	3	AAA14039	Aaa14039 Human liv
c	18	20	0.7	20	3	AAA14041	Aaa14041 Human liv
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c	20	20	0.7	20	3	AAA14011	Aaa14011 Human liv
c	21	20	0.7	20	3	AAA14029	Aaa14029 Human liv
c	22	20	0.7	20	3	AAA14044	Aaa14044 Human liv
c	23	20	0.7	20	3	AAA14047	Aaa14047 Human liv
c	24	20	0.7	20	3	AAA14015	Aaa14015 Human liv
c	25	20	0.7	20	3	AAA14008	Aaa14008 Human liv
c	26	20	0.7	20	3	AAA14009	Aaa14009 Human liv
c	27	20	0.7	20	3	AAA14012	Aaa14012 Human liv
c	28	20	0.7	20	3	AAA14022	Aaa14022 Human liv
c	29	20	0.7	20	3	AAA14026	Aaa14026 Human liv
c	30	20	0.7	20	3	AAA14036	Aaa14036 Human liv
c	31	20	0.7	20	3	AAA14019	Aaa14019 Human liv
c	32	20	0.7	20	3	AAA14033	Aaa14033 Human liv
c	33	20	0.7	20	3	AAA14028	Aaa14028 Human liv
c	34	20	0.7	20	3	AAA14040	Aaa14040 Human liv
c	35	20	0.7	20	3	AAA14014	Aaa14014 Human liv
c	36	20	0.7	20	3	AAA14016	Aaa14016 Human liv
c	37	20	0.7	20	3	AAA14024	Aaa14024 Human liv
c	38	20	0.7	20	3	AAA14031	Aaa14031 Human liv
c	39	20	0.7	20	3	AAA14035	Aaa14035 Human liv
c	40	20	0.7	20	3	AAA14021	Aaa14021 Human liv
c	41	20	0.7	20	3	AAA14038	Aaa14038 Human liv
c	42	20	0.7	20	3	AAA14013	Aaa14013 Human liv
c	43	20	0.7	20	3	AAA14017	Aaa14017 Human liv
c	44	20	0.7	20	3	AAA14025	Aaa14025 Human liv
c	45	20	0.7	20	3	AAA14032	Aaa14032 Human liv

ALIGNMENTS

RESULT 1
AAA14004
ID AAA14004 standard; DNA; 27 BP.
XX
AC AAA14004;
XX
DT 18-JUL-2000 (first entry)
XX
DE Human liver glycogen phosphorylase quantitative real-time PCR probe #4.
XX
KW Liver glycogen phosphorylase; PYGL gene; human; chromosome 14;
KW 1,4-alpha-D-glucan:orthophosphate alpha-D-glucosyltransferase; HGLPa;
KW glycogenolysis; carbohydrate metabolism; blood glucose homeostasis;
KW expression inhibition; antisense therapy; hypoglycaemic;
KW type II diabetes; non insulin-dependent;
KW quantitative real-time PCR probe; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1
FT /*tag= a
FT /note= "Conjugated to fluorescent reporter dye FAM"
FT modified_base 27
FT /*tag= b
FT /note= "Conjugated to fluorescent quencher dye TAMRA"
XX
PN US6043091-A.
XX
PD 28-MAR-2000.
XX
PF 19-JUL-1999; 99US-00357071.
XX
PR 19-JUL-1999; 99US-00357071.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Cowsert LM;
XX
DR WPI; 2000-270346/23.
XX
PT Antisense compounds particularly oligonucleotides useful for prophylaxis,
PT diagnosis and treatment of diseases associated with expression of liver
PT glycogen phosphorylase.
XX
PS Example 13; Col 38; 33pp; English.

```
XX
CC   This sequence represents a human liver glycogen phosphorylase probe used
CC   in quantitative real-time PCR with primers AAA14002-A14003 in an
CC   exemplification of the present invention. The invention relates to
CC   antisense oligonucleotides targetted to the human liver glycogen
CC   phosphorylase gene (PYGL gene), which inhibit its expression. A series of
CC   oligonucleotides (AAA14008-A14047) were designed to target different
CC   regions of human liver glycogen phosphorylase RNA, and were analysed for
CC   their effect on liver glycogen phosphorylase levels by quantitative real-
CC   time PCR. GAPDH (glyceraldehyde-3-phosphate) mRNA levels were measured as
CC   a control. Liver glycogen phosphorylase is one of three glycogen
CC   phosphorylase isozymes, which differ in their tissue-specific
CC   distribution, immunological properties and electrophoretic mobilities and
CC   are encoded by three different genes. Liver glycogen phosphorylase is
CC   encoded by the PYGL gene, which is located on chromosome 14. Liver
CC   glycogen phosphorylase (also known as 1,4-alpha-D-glucan:orthophosphate
CC   alpha-D-glucosyltransferase, and HGLPa in its phosphorylated, active
CC   form) catalyses the degradation of stored glycogen in the liver to
CC   glucose-1-phosphate via the cleavage of the alpha-1,4-glycosidic bonds.
CC   It therefore plays a critical role in carbohydrate metabolism and blood
CC   glucose homeostasis. Inhibition of liver glycogen phosphorylase and
CC   therefore glycogenolysis may provide a means of reducing blood glucose
CC   levels in diabetic patients, particularly those with type II (non insulin
CC   -dependent) diabetes. The antisense oligonucleotides of the invention are
CC   useful for diagnosis, prevention and treatment of conditions associated
CC   with liver glycogen phosphorylase expression, or those which may benefit
CC   from inhibition of liver glycogen phosphorylase expression, such as type
CC   II diabetes
XX
SQ   Sequence 27 BP; 5 A; 6 C; 8 G; 8 T; 0 U; 0 Other;

  Query Match             1.0%;  Score 27;  DB 3;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 3.3e+03;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        437 CTGTGATGAGGCCATTTACCAGCTTGG 463
              |||||||||||||||||||||||||||
Db          1 CTGTGATGAGGCCATTTACCAGCTTGG 27


RESULT 2
AAA14003/c
ID   AAA14003 standard; DNA; 21 BP.
XX
AC   AAA14003;
XX
DT   18-JUL-2000  (first entry)
XX
DE   Human liver glycogen phosphorylase quantitative real-time PCR primer #3.
XX
KW   Liver glycogen phosphorylase; PYGL gene; human; chromosome 14;
KW   1,4-alpha-D-glucan:orthophosphate alpha-D-glucosyltransferase; HGLPa;
KW   glycogenolysis; carbohydrate metabolism; blood glucose homeostasis;
KW   expression inhibition; antisense therapy; hypoglycaemic;
KW   type II diabetes; non insulin-dependent;
KW   quantitative real-time PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   US6043091-A.
XX
PD   28-MAR-2000.
XX
PF   19-JUL-1999;   99US-00357071.
XX
PR   19-JUL-1999;   99US-00357071.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Monia BP,  Cowsert LM;
XX
DR   WPI; 2000-270346/23.
XX
PT   Antisense compounds particularly oligonucleotides useful for prophylaxis,
PT   diagnosis and treatment of diseases associated with expression of liver
PT   glycogen phosphorylase.
XX
PS   Example 13; Col 38; 33pp; English.
XX
CC   Sequences AAA14002-A14003 represent human liver glycogen phosphorylase
CC   PCR primers used in quantitative real-time PCR with probe AAA14003 in an
CC   exemplification of the present invention. The invention relates to
CC   antisense oligonucleotides targetted to the human liver glycogen
CC   phosphorylase gene (PYGL gene), which inhibit its expression. A series of
CC   oligonucleotides (AAA14008-A14047) were designed to target different
CC   regions of human liver glycogen phosphorylase RNA, and were analysed for
CC   their effect on liver glycogen phosphorylase levels by quantitative real-
CC   time PCR. GAPDH (glyceraldehyde-3-phosphate) mRNA levels were measured as
CC   a control. Liver glycogen phosphorylase is one of three glycogen
CC   phosphorylase isozymes, which differ in their tissue-specific
CC   distribution, immunological properties and electrophoretic mobilities and
CC   are encoded by three different genes. Liver glycogen phosphorylase is
CC   encoded by the PYGL gene, which is located on chromosome 14. Liver
CC   glycogen phosphorylase (also known as 1,4-alpha-D-glucan:orthophosphate
CC   alpha-D-glucosyltransferase, and HGLPa in its phosphorylated, active
CC   form) catalyses the degradation of stored glycogen in the liver to
CC   glucose-1-phosphate via the cleavage of the alpha-1,4-glycosidic bonds.
CC   It therefore plays a critical role in carbohydrate metabolism and blood
CC   glucose homeostasis. Inhibition of liver glycogen phosphorylase and
CC   therefore glycogenolysis may provide a means of reducing blood glucose
CC   levels in diabetic patients, particularly those with type II (non insulin
CC   -dependent) diabetes. The antisense oligonucleotides of the invention are
CC   useful for diagnosis, prevention and treatment of conditions associated
CC   with liver glycogen phosphorylase expression, or those which may benefit
CC   from inhibition of liver glycogen phosphorylase expression, such as type
CC   II diabetes
XX
SQ   Sequence 21 BP; 7 A; 8 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 21;  DB 3;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+05;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        505 GACTTGGCAATGGTGGTCTTG 525
              |||||||||||||||||||||
Db         21 GACTTGGCAATGGTGGTCTTG 1


RESULT 3
AAA14002
ID   AAA14002 standard; DNA; 21 BP.
XX
AC   AAA14002;
XX
DT   18-JUL-2000  (first entry)
XX
DE   Human liver glycogen phosphorylase quantitative real-time PCR primer #2.
XX
KW   Liver glycogen phosphorylase; PYGL gene; human; chromosome 14;
KW   1,4-alpha-D-glucan:orthophosphate alpha-D-glucosyltransferase; HGLPa;
KW   glycogenolysis; carbohydrate metabolism; blood glucose homeostasis;
KW   expression inhibition; antisense therapy; hypoglycaemic;
KW   type II diabetes; non insulin-dependent;
KW   quantitative real-time PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   US6043091-A.
XX
PD   28-MAR-2000.
XX
PF   19-JUL-1999;   99US-00357071.
XX
PR   19-JUL-1999;   99US-00357071.
XX
PA   (ISIS-) ISIS PHARM INC.
```

XX
PI Monia BP, Cowsert LM;
XX
DR WPI; 2000-270346/23.
XX
PT Antisense compounds particularly oligonucleotides useful for prophylaxis,
PT diagnosis and treatment of diseases associated with expression of liver
PT glycogen phosphorylase.
XX
PS Example 13; Col 38; 33pp; English.
XX
CC Sequences AAA14002-A14003 represent human liver glycogen phosphorylase
CC PCR primers used in quantitative real-time PCR with probe AAA14003 in an
CC exemplification of the present invention. The invention relates to
CC antisense oligonucleotides targetted to the human liver glycogen
CC phosphorylase gene (PYGL gene), which inhibit its expression. A series of
CC oligonucleotides (AAA14008-A14047) were designed to target different
CC regions of human liver glycogen phosphorylase RNA, and were analysed for
CC their effect on liver glycogen phosphorylase levels by quantitative real-
CC time PCR. GAPDH (glyceraldehyde-3-phosphate) mRNA levels were measured as
CC a control. Liver glycogen phosphorylase is one of three glycogen
CC phosphorylase isozymes, which differ in their tissue-specific
CC distribution, immunological properties and electrophoretic mobilities and
CC are encoded by three different genes. Liver glycogen phosphorylase is
CC encoded by the PYGL gene, which is located on chromosome 14. Liver
CC glycogen phosphorylase (also known as 1,4-alpha-D-glucan:orthophosphate
CC alpha-D-glucosyltransferase, and HGLPa in its phosphorylated, active
CC form) catalyses the degradation of stored glycogen in the liver to
CC glucose-1-phosphate via the cleavage of the alpha-1,4-glycosidic bonds.
CC It therefore plays a critical role in carbohydrate metabolism and blood
CC glucose homeostasis. Inhibition of liver glycogen phosphorylase and
CC therefore glycogenolysis may provide a means of reducing blood glucose
CC levels in diabetic patients, particularly those with type II (non insulin
CC -dependent) diabetes. The antisense oligonucleotides of the invention are
CC useful for diagnosis, prevention and treatment of conditions associated
CC with liver glycogen phosphorylase expression, or those which may benefit
CC from inhibition of liver glycogen phosphorylase expression, such as type
CC II diabetes
XX
SQ Sequence 21 BP; 8 A; 5 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 0.7%; Score 21; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 386 CATGGGCCGAACATTACAGAA 406
||||||||||||||||||||
Db 1 CATGGGCCGAACATTACAGAA 21

RESULT 4
AAF97019
ID AAF97019 standard; DNA; 21 BP.
XX
AC AAF97019;
XX
DT 06-JUN-2001 (first entry)
XX
DE Human gene single nucleotide polymorphism #1780.
XX
KW Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
KW polymorphism; vascular disease; coronary artery disease; forensics;
KW myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
KW pulmonary embolism; paternity test; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Variation replace(11,G)
FT /*tag= a
FT /standard_name= "single nucleotide polymorphism"
XX
PN WO200118250-A2.
XX
PD 15-MAR-2001.
XX
PF 07-SEP-2000; 2000WO-US024503.
XX
PR 10-SEP-1999; 99US-0153357P.
PR 26-JUL-2000; 2000US-0220947P.
PR 16-AUG-2000; 2000US-0225724P.
XX
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, Mccarthy JJ;
XX
DR WPI; 2001-226749/23.
XX
PT Nucleic acids comprising single nucleotide polymorphisms, useful in
PT applications such as forensics, paternity testing, medicine, genetic
PT analysis and phenotype correlations to diseases such as diabetes and
PT atherosclerosis.
XX
PS Example; Page 166; 242pp; English.
XX
CC The present invention provides a method of diagnosing a vascular disease
CC in an individual, involving determining the sequence at various
CC polymorphic sites within the human thrombospondin 1 and thrombospondin 4
CC genes. The sequences at a number of polymorphic sites are also provided
CC in the specification. In particular, the method can be used in the
CC diagnosis of atherosclerosis, myocardial infarction, coronary heart
CC disease, stroke, peripheral vascular diseases, venous thromboembolism and
CC pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
CC useful in forensics, paternity testing, genetic analysis and phenotype
CC correlations to diseases. The present sequence is an example of one of
CC the human gene SNPS shown in the specification
XX
SQ Sequence 21 BP; 5 A; 4 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 0.7%; Score 21; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1377 GATGTGGACCCTCTGAGAAGG 1397
||||||||||||||||||||
Db 1 GATGTGGACCCTCTGAGAAGG 21

RESULT 5
AAF97017
ID AAF97017 standard; DNA; 21 BP.
XX
AC AAF97017;
XX
DT 06-JUN-2001 (first entry)
XX
DE Human gene single nucleotide polymorphism #1778.
XX
KW Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
KW polymorphism; vascular disease; coronary artery disease; forensics;
KW myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
KW pulmonary embolism; paternity test; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Variation replace(11,T)
FT /*tag= a
FT /standard_name= "single nucleotide polymorphism"
XX
PN WO200118250-A2.
XX
PD 15-MAR-2001.
XX
PF 07-SEP-2000; 2000WO-US024503.

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XX
PR   10-SEP-1999;   99US-0153357P.
PR   26-JUL-2000; 2000US-0220947P.
PR   16-AUG-2000; 2000US-0225724P.
XX
PA   (WHED ) WHITEHEAD INST BIOMEDICAL RES.
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Lander ES,  Gargill M,  Ireland JS,  Bolk S,  Daley GQ,  Mccarthy JJ;
XX
DR   WPI; 2001-226749/23.
XX
PT   Nucleic acids comprising single nucleotide polymorphisms, useful in
PT   applications such as forensics, paternity testing, medicine, genetic
PT   analysis and phenotype correlations to diseases such as diabetes and
PT   atherosclerosis.
XX
PS   Example; Page 166; 242pp; English.
XX
CC   The present invention provides a method of diagnosing a vascular disease
CC   in an individual, involving determining the sequence at various
CC   polymorphic sites within the human thrombospondin 1 and thrombospondin 4
CC   genes. The sequences at a number of polymorphic sites are also provided
CC   in the specification. In particular, the method can be used in the
CC   diagnosis of atherosclerosis, myocardial infarction, coronary heart
CC   disease, stroke, peripheral vascular diseases, venous thromboembolism and
CC   pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
CC   useful in forensics, paternity testing, genetic analysis and phenotype
CC   correlations to diseases. The present sequence is an example of one of
CC   the human gene SNPS shown in the specification
XX
SQ   Sequence 21 BP; 9 A; 4 C; 4 G; 4 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 21;  DB 4;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+05;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1873 TGTACAACCGCATTAAGAAAG 1893
              |||||||||||||||||||||
Db          1 TGTACAACCGCATTAAGAAAG 21


RESULT 6
AAF97016
ID   AAF97016 standard; DNA; 21 BP.
XX
AC   AAF97016;
XX
DT   06-JUN-2001  (first entry)
XX
DE   Human gene single nucleotide polymorphism #1777.
XX
KW   Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
KW   polymorphism; vascular disease; coronary artery disease; forensics;
KW   myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
KW   pulmonary embolism; paternity test; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Variation       replace(11,C)
FT                   /*tag=  a
FT                   /standard_name= "single nucleotide polymorphism"
XX
PN   WO200118250-A2.
XX
PD   15-MAR-2001.
XX
PF   07-SEP-2000; 2000WO-US024503.
XX
PR   10-SEP-1999;   99US-0153357P.
PR   26-JUL-2000; 2000US-0220947P.
PR   16-AUG-2000; 2000US-0225724P.
XX
PA   (WHED ) WHITEHEAD INST BIOMEDICAL RES.
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Lander ES,  Gargill M,  Ireland JS,  Bolk S,  Daley GQ,  Mccarthy JJ;
XX
DR   WPI; 2001-226749/23.
XX
PT   Nucleic acids comprising single nucleotide polymorphisms, useful in
PT   applications such as forensics, paternity testing, medicine, genetic
PT   analysis and phenotype correlations to diseases such as diabetes and
PT   atherosclerosis.
XX
PS   Example; Page 166; 242pp; English.
XX
CC   The present invention provides a method of diagnosing a vascular disease
CC   in an individual, involving determining the sequence at various
CC   polymorphic sites within the human thrombospondin 1 and thrombospondin 4
CC   genes. The sequences at a number of polymorphic sites are also provided
CC   in the specification. In particular, the method can be used in the
CC   diagnosis of atherosclerosis, myocardial infarction, coronary heart
CC   disease, stroke, peripheral vascular diseases, venous thromboembolism and
CC   pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
CC   useful in forensics, paternity testing, genetic analysis and phenotype
CC   correlations to diseases. The present sequence is an example of one of
CC   the human gene SNPS shown in the specification
XX
SQ   Sequence 21 BP; 5 A; 5 C; 6 G; 5 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 21;  DB 4;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+05;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1978 AGCTGATCACTTCAGTGGCAG 1998
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Db          1 AGCTGATCACTTCAGTGGCAG 21


RESULT 7
AAF97015
ID   AAF97015 standard; DNA; 21 BP.
XX
AC   AAF97015;
XX
DT   06-JUN-2001  (first entry)
XX
DE   Human gene single nucleotide polymorphism #1776.
XX
KW   Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
KW   polymorphism; vascular disease; coronary artery disease; forensics;
KW   myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
KW   pulmonary embolism; paternity test; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Variation       replace(11,C)
FT                   /*tag=  a
FT                   /standard_name= "single nucleotide polymorphism"
XX
PN   WO200118250-A2.
XX
PD   15-MAR-2001.
XX
PF   07-SEP-2000; 2000WO-US024503.
XX
PR   10-SEP-1999;   99US-0153357P.
PR   26-JUL-2000; 2000US-0220947P.
PR   16-AUG-2000; 2000US-0225724P.
XX
PA   (WHED ) WHITEHEAD INST BIOMEDICAL RES.
PA   (MILL-) MILLENNIUM PHARM INC.
XX
```

PI Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, Mccarthy JJ;
XX
DR WPI; 2001-226749/23.
XX
PT Nucleic acids comprising single nucleotide polymorphisms, useful in
PT applications such as forensics, paternity testing, medicine, genetic
PT analysis and phenotype correlations to diseases such as diabetes and
PT atherosclerosis.
XX
PS Example; Page 166; 242pp; English.
XX
CC The present invention provides a method of diagnosing a vascular disease
CC in an individual, involving determining the sequence at various
CC polymorphic sites within the human thrombospondin 1 and thrombospondin 4
CC genes. The sequences at a number of polymorphic sites are also provided
CC in the specification. In particular, the method can be used in the
CC diagnosis of atherosclerosis, myocardial infarction, coronary heart
CC disease, stroke, peripheral vascular diseases, venous thromboembolism and
CC pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
CC useful in forensics, paternity testing, genetic analysis and phenotype
CC correlations to diseases. The present sequence is an example of one of
CC the human gene SNPS shown in the specification
XX
SQ Sequence 21 BP; 6 A; 7 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 0.7%; Score 21; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1123 AGCTGAATGATACTCACCCTC 1143
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Db 1 AGCTGAATGATACTCACCCTC 21

RESULT 8
AAF97018
ID AAF97018 standard; DNA; 21 BP.
XX
AC AAF97018;
XX
DT 06-JUN-2001 (first entry)
XX
DE Human gene single nucleotide polymorphism #1779.
XX
KW Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
KW polymorphism; vascular disease; coronary artery disease; forensics;
KW myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
KW pulmonary embolism; paternity test; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Variation replace(11,G)
FT /*tag= a
FT /standard_name= "single nucleotide polymorphism"
XX
PN WO200118250-A2.
XX
PD 15-MAR-2001.
XX
PF 07-SEP-2000; 2000WO-US024503.
XX
PR 10-SEP-1999; 99US-0153357P.
PR 26-JUL-2000; 2000US-0220947P.
PR 16-AUG-2000; 2000US-0225724P.
XX
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, Mccarthy JJ;
XX
DR WPI; 2001-226749/23.
XX
PT Nucleic acids comprising single nucleotide polymorphisms, useful in
PT applications such as forensics, paternity testing, medicine, genetic
PT analysis and phenotype correlations to diseases such as diabetes and
PT atherosclerosis.
XX
PS Example; Page 166; 242pp; English.
XX
CC The present invention provides a method of diagnosing a vascular disease
CC in an individual, involving determining the sequence at various
CC polymorphic sites within the human thrombospondin 1 and thrombospondin 4
CC genes. The sequences at a number of polymorphic sites are also provided
CC in the specification. In particular, the method can be used in the
CC diagnosis of atherosclerosis, myocardial infarction, coronary heart
CC disease, stroke, peripheral vascular diseases, venous thromboembolism and
CC pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
CC useful in forensics, paternity testing, genetic analysis and phenotype
CC correlations to diseases. The present sequence is an example of one of
CC the human gene SNPS shown in the specification
XX
SQ Sequence 21 BP; 8 A; 3 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 0.7%; Score 21; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 AAGCAAGTTGAAAGTCATCTT 21

RESULT 9
AAH62165
ID AAH62165 standard; DNA; 21 BP.
XX
AC AAH62165;
XX
DT 12-SEP-2001 (first entry)
XX
DE Phosphorylaes glycogen polymorphism containng DNA fragment #66.
XX
KW Single nucleotide polymorphism; SNP; human; cancer; inflammation;
KW heart disease; paternity testing; forensic science; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Variation replace(11,G)
FT /*tag= a
FT /standard_name= "single nucleotide polymorphism"
XX
PN WO200138576-A2.
XX
PD 31-MAY-2001.
XX
PF 17-NOV-2000; 2000WO-US031639.
XX
PR 24-NOV-1999; 99US-0167334P.
XX
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
XX
PI Cargill M, Ireland JS, Lander ES;
XX
DR WPI; 2001-367705/38.
XX
PT New nucleic acid segments of the human genome, particularly from genes
PT including polymorphic sites,for phenotype correlation, forensics,
PT paternity testing, medicine and genetic analysis.
XX
PS Claim 1; Page 34; 80pp; English.
XX
CC DNA sequences AAH62100 - AAH62688 represent segments of human genes which
CC contain single nucleotide polymorphisms (SNPs). A method is included in
CC the invention for analysing a nucleic acid sample, which consists of

CC determining the base occupying any one of the polymorphic sites given in
CC the SNP containing sequences. The nucleotide sequences can be used in the
CC diagnosis or monitoring of diseases, such as cancer, inflammation, heart
CC diseases, diseases of the cardiovascular system, and infection by
CC microorganisms. The oligonucleotides are also useful in the manufacture
CC of a medicament for the treatment or prophylaxis of the diseases, and as
CC a pharmaceutical. SNP containing oligonucleotides are useful in
CC applications such as phenotype correlation, forensics, paternity testing,
CC medicine and genetic analysis
XX
SQ Sequence 21 BP; 7 A; 8 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 0.7%; Score 21; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1218 AACCAGAAGACCTTCGCCTAC 1238
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Db 1 AACCAGAAGACCTTCGCCTAC 21

RESULT 10
AAH62170
ID AAH62170 standard; DNA; 21 BP.
XX
AC AAH62170;
XX
DT 12-SEP-2001 (first entry)
XX
DE Phosphorylaes glycogen polymorphism containng DNA fragment #71.
XX
KW Single nucleotide polymorphism; SNP; human; cancer; inflammation;
KW heart disease; paternity testing; forensic science; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Variation replace(11,A)
FT /*tag= a
FT /standard_name= "single nucleotide polymorphism"
XX
PN WO200138576-A2.
XX
PD 31-MAY-2001.
XX
PF 17-NOV-2000; 2000WO-US031639.
XX
PR 24-NOV-1999; 99US-0167334P.
XX
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
XX
PI Cargill M, Ireland JS, Lander ES;
XX
DR WPI; 2001-367705/38.
XX
PT New nucleic acid segments of the human genome, particularly from genes
PT including polymorphic sites,for phenotype correlation, forensics,
PT paternity testing, medicine and genetic analysis.
XX
PS Claim 1; Page 35; 80pp; English.
XX
CC DNA sequences AAH62100 - AAH62688 represent segments of human genes which
CC contain single nucleotide polymorphisms (SNPs). A method is included in
CC the invention for analysing a nucleic acid sample, which consists of
CC determining the base occupying any one of the polymorphic sites given in
CC the SNP containing sequences. The nucleotide sequences can be used in the
CC diagnosis or monitoring of diseases, such as cancer, inflammation, heart
CC diseases, diseases of the cardiovascular system, and infection by
CC microorganisms. The oligonucleotides are also useful in the manufacture
CC of a medicament for the treatment or prophylaxis of the diseases, and as
CC a pharmaceutical. SNP containing oligonucleotides are useful in
CC applications such as phenotype correlation, forensics, paternity testing,
CC medicine and genetic analysis
XX
SQ Sequence 21 BP; 8 A; 3 C; 9 G; 1 T; 0 U; 0 Other;

Query Match 0.7%; Score 21; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GGACAAGAAAGGGTACGAGGC 21

RESULT 11
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ID AAH62169 standard; DNA; 21 BP.
XX
AC AAH62169;
XX
DT 12-SEP-2001 (first entry)
XX
DE Phosphorylaes glycogen polymorphism containng DNA fragment #70.
XX
KW Single nucleotide polymorphism; SNP; human; cancer; inflammation;
KW heart disease; paternity testing; forensic science; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Variation replace(11,A)
FT /*tag= a
FT /standard_name= "single nucleotide polymorphism"
XX
PN WO200138576-A2.
XX
PD 31-MAY-2001.
XX
PF 17-NOV-2000; 2000WO-US031639.
XX
PR 24-NOV-1999; 99US-0167334P.
XX
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
XX
PI Cargill M, Ireland JS, Lander ES;
XX
DR WPI; 2001-367705/38.
XX
PT New nucleic acid segments of the human genome, particularly from genes
PT including polymorphic sites,for phenotype correlation, forensics,
PT paternity testing, medicine and genetic analysis.
XX
PS Claim 1; Page 35; 80pp; English.
XX
CC DNA sequences AAH62100 - AAH62688 represent segments of human genes which
CC contain single nucleotide polymorphisms (SNPs). A method is included in
CC the invention for analysing a nucleic acid sample, which consists of
CC determining the base occupying any one of the polymorphic sites given in
CC the SNP containing sequences. The nucleotide sequences can be used in the
CC diagnosis or monitoring of diseases, such as cancer, inflammation, heart
CC diseases, diseases of the cardiovascular system, and infection by
CC microorganisms. The oligonucleotides are also useful in the manufacture
CC of a medicament for the treatment or prophylaxis of the diseases, and as
CC a pharmaceutical. SNP containing oligonucleotides are useful in
CC applications such as phenotype correlation, forensics, paternity testing,
CC medicine and genetic analysis
XX
SQ Sequence 21 BP; 6 A; 3 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 0.7%; Score 21; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2269 TGGCTGCTTTGGACAAGAAAG 2289
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Db          1 TGGCTGCTTTGGACAAGAAAG 21


RESULT 12
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ID   AAH62167 standard; DNA; 21 BP.
XX
AC   AAH62167;
XX
DT   12-SEP-2001  (first entry)
XX
DE   Phosphorylaes glycogen polymorphism containng DNA fragment #68.
XX
KW   Single nucleotide polymorphism; SNP; human; cancer; inflammation;
KW   heart disease; paternity testing; forensic science; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Variation       replace(11,A)
FT                   /*tag=  a
FT                   /standard_name= "single nucleotide polymorphism"
XX
PN   WO200138576-A2.
XX
PD   31-MAY-2001.
XX
PF   17-NOV-2000; 2000WO-US031639.
XX
PR   24-NOV-1999;   99US-0167334P.
XX
PA   (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX
PI   Cargill M,  Ireland JS,  Lander ES;
XX
DR   WPI; 2001-367705/38.
XX
PT   New nucleic acid segments of the human genome, particularly from genes
PT   including polymorphic sites,for phenotype correlation, forensics,
PT   paternity testing, medicine and genetic analysis.
XX
PS   Claim 1; Page 34; 80pp; English.
XX
CC   DNA sequences AAH62100 - AAH62688 represent segments of human genes which
CC   contain single nucleotide polymorphisms (SNPs). A method is included in
CC   the invention for analysing a nucleic acid sample, which consists of
CC   determining the base occupying any one of the polymorphic sites given in
CC   the SNP containing sequences. The nucleotide sequences can be used in the
CC   diagnosis or monitoring of diseases, such as cancer, inflammation, heart
CC   diseases, diseases of the cardiovascular system, and infection by
CC   microorganisms. The oligonucleotides are also useful in the manufacture
CC   of a medicament for the treatment or prophylaxis of the diseases, and as
CC   a pharmaceutical. SNP containing oligonucleotides are useful in
CC   applications such as phenotype correlation, forensics, paternity testing,
CC   medicine and genetic analysis
XX
SQ   Sequence 21 BP; 6 A; 4 C; 6 G; 5 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 21;  DB 4;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+05;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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              |||||||||||||||||||||
Db          1 GGTGAACAATGACCCTATGGT 21


RESULT 13
AAH62171
ID   AAH62171 standard; DNA; 21 BP.
XX
AC   AAH62171;
XX
DT   12-SEP-2001  (first entry)
XX
DE   Phosphorylaes glycogen polymorphism containng DNA fragment #72.
XX
KW   Single nucleotide polymorphism; SNP; human; cancer; inflammation;
KW   heart disease; paternity testing; forensic science; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Variation       replace(11,T)
FT                   /*tag=  a
FT                   /standard_name= "single nucleotide polymorphism"
XX
PN   WO200138576-A2.
XX
PD   31-MAY-2001.
XX
PF   17-NOV-2000; 2000WO-US031639.
XX
PR   24-NOV-1999;   99US-0167334P.
XX
PA   (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX
PI   Cargill M,  Ireland JS,  Lander ES;
XX
DR   WPI; 2001-367705/38.
XX
PT   New nucleic acid segments of the human genome, particularly from genes
PT   including polymorphic sites,for phenotype correlation, forensics,
PT   paternity testing, medicine and genetic analysis.
XX
PS   Claim 1; Page 35; 80pp; English.
XX
CC   DNA sequences AAH62100 - AAH62688 represent segments of human genes which
CC   contain single nucleotide polymorphisms (SNPs). A method is included in
CC   the invention for analysing a nucleic acid sample, which consists of
CC   determining the base occupying any one of the polymorphic sites given in
CC   the SNP containing sequences. The nucleotide sequences can be used in the
CC   diagnosis or monitoring of diseases, such as cancer, inflammation, heart
CC   diseases, diseases of the cardiovascular system, and infection by
CC   microorganisms. The oligonucleotides are also useful in the manufacture
CC   of a medicament for the treatment or prophylaxis of the diseases, and as
CC   a pharmaceutical. SNP containing oligonucleotides are useful in
CC   applications such as phenotype correlation, forensics, paternity testing,
CC   medicine and genetic analysis
XX
SQ   Sequence 21 BP; 3 A; 4 C; 3 G; 11 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 21;  DB 4;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+05;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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              |||||||||||||||||||||
Db          1 TTGACAATGGCTTTTTTTCTC 21


RESULT 14
AAH62166
ID   AAH62166 standard; DNA; 21 BP.
XX
AC   AAH62166;
XX
DT   12-SEP-2001  (first entry)
XX
DE   Phosphorylaes glycogen polymorphism containng DNA fragment #67.
XX
KW   Single nucleotide polymorphism; SNP; human; cancer; inflammation;
KW   heart disease; paternity testing; forensic science; ds.
XX
OS   Homo sapiens.
XX
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FH   Key             Location/Qualifiers
FT   Variation       replace(11,A)
FT                   /*tag=  a
FT                   /standard_name= "single nucleotide polymorphism"
XX
PN   WO200138576-A2.
XX
PD   31-MAY-2001.
XX
PF   17-NOV-2000; 2000WO-US031639.
XX
PR   24-NOV-1999;   99US-0167334P.
XX
PA   (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX
PI   Cargill M,  Ireland JS,  Lander ES;
XX
DR   WPI; 2001-367705/38.
XX
PT   New nucleic acid segments of the human genome, particularly from genes
PT   including polymorphic sites,for phenotype correlation, forensics,
PT   paternity testing, medicine and genetic analysis.
XX
PS   Claim 1; Page 34; 80pp; English.
XX
CC   DNA sequences AAH62100 - AAH62688 represent segments of human genes which
CC   contain single nucleotide polymorphisms (SNPs). A method is included in
CC   the invention for analysing a nucleic acid sample, which consists of
CC   determining the base occupying any one of the polymorphic sites given in
CC   the SNP containing sequences. The nucleotide sequences can be used in the
CC   diagnosis or monitoring of diseases, such as cancer, inflammation, heart
CC   diseases, diseases of the cardiovascular system, and infection by
CC   microorganisms. The oligonucleotides are also useful in the manufacture
CC   of a medicament for the treatment or prophylaxis of the diseases, and as
CC   a pharmaceutical. SNP containing oligonucleotides are useful in
CC   applications such as phenotype correlation, forensics, paternity testing,
CC   medicine and genetic analysis
XX
SQ   Sequence 21 BP; 4 A; 8 C; 6 G; 3 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 21;  DB 4;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+05;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          1 CCTCCGGGAACTCGCCAAGGT 21


RESULT 15
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ID   AAH62168 standard; DNA; 21 BP.
XX
AC   AAH62168;
XX
DT   12-SEP-2001  (first entry)
XX
DE   Phosphorylaes glycogen polymorphism containng DNA fragment #69.
XX
KW   Single nucleotide polymorphism; SNP; human; cancer; inflammation;
KW   heart disease; paternity testing; forensic science; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Variation       replace(11,T)
FT                   /*tag=  a
FT                   /standard_name= "single nucleotide polymorphism"
XX
PN   WO200138576-A2.
XX
PD   31-MAY-2001.
XX
PF   17-NOV-2000; 2000WO-US031639.
XX
PR   24-NOV-1999;   99US-0167334P.
XX
PA   (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX
PI   Cargill M,  Ireland JS,  Lander ES;
XX
DR   WPI; 2001-367705/38.
XX
PT   New nucleic acid segments of the human genome, particularly from genes
PT   including polymorphic sites,for phenotype correlation, forensics,
PT   paternity testing, medicine and genetic analysis.
XX
PS   Claim 1; Page 35; 80pp; English.
XX
CC   DNA sequences AAH62100 - AAH62688 represent segments of human genes which
CC   contain single nucleotide polymorphisms (SNPs). A method is included in
CC   the invention for analysing a nucleic acid sample, which consists of
CC   determining the base occupying any one of the polymorphic sites given in
CC   the SNP containing sequences. The nucleotide sequences can be used in the
CC   diagnosis or monitoring of diseases, such as cancer, inflammation, heart
CC   diseases, diseases of the cardiovascular system, and infection by
CC   microorganisms. The oligonucleotides are also useful in the manufacture
CC   of a medicament for the treatment or prophylaxis of the diseases, and as
CC   a pharmaceutical. SNP containing oligonucleotides are useful in
CC   applications such as phenotype correlation, forensics, paternity testing,
CC   medicine and genetic analysis
XX
SQ   Sequence 21 BP; 4 A; 8 C; 7 G; 2 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 21;  DB 4;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+05;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          1 CTGCAGGCACCGAAGCCTCGG 21


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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c	8	20	0.7	20	3	US-09-357-071-12	Sequence 12, Appl
c	9	20	0.7	20	3	US-09-357-071-13	Sequence 13, Appl
c	10	20	0.7	20	3	US-09-357-071-14	Sequence 14, Appl
c	11	20	0.7	20	3	US-09-357-071-15	Sequence 15, Appl
c	12	20	0.7	20	3	US-09-357-071-16	Sequence 16, Appl
c	13	20	0.7	20	3	US-09-357-071-17	Sequence 17, Appl
c	14	20	0.7	20	3	US-09-357-071-18	Sequence 18, Appl
c	15	20	0.7	20	3	US-09-357-071-19	Sequence 19, Appl
c	16	20	0.7	20	3	US-09-357-071-20	Sequence 20, Appl
c	17	20	0.7	20	3	US-09-357-071-21	Sequence 21, Appl
c	18	20	0.7	20	3	US-09-357-071-22	Sequence 22, Appl
c	19	20	0.7	20	3	US-09-357-071-23	Sequence 23, Appl
c	20	20	0.7	20	3	US-09-357-071-24	Sequence 24, Appl
c	21	20	0.7	20	3	US-09-357-071-25	Sequence 25, Appl
c	22	20	0.7	20	3	US-09-357-071-26	Sequence 26, Appl
c	23	20	0.7	20	3	US-09-357-071-27	Sequence 27, Appl
c	24	20	0.7	20	3	US-09-357-071-28	Sequence 28, Appl
c	25	20	0.7	20	3	US-09-357-071-29	Sequence 29, Appl
c	26	20	0.7	20	3	US-09-357-071-30	Sequence 30, Appl
c	27	20	0.7	20	3	US-09-357-071-31	Sequence 31, Appl
c	28	20	0.7	20	3	US-09-357-071-32	Sequence 32, Appl
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c	30	20	0.7	20	3	US-09-357-071-34	Sequence 34, Appl
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c	32	20	0.7	20	3	US-09-357-071-36	Sequence 36, Appl
c	33	20	0.7	20	3	US-09-357-071-37	Sequence 37, Appl
c	34	20	0.7	20	3	US-09-357-071-38	Sequence 38, Appl
c	35	20	0.7	20	3	US-09-357-071-39	Sequence 39, Appl
c	36	20	0.7	20	3	US-09-357-071-40	Sequence 40, Appl
c	37	20	0.7	20	3	US-09-357-071-41	Sequence 41, Appl
c	38	20	0.7	20	3	US-09-357-071-42	Sequence 42, Appl
c	39	20	0.7	20	3	US-09-357-071-43	Sequence 43, Appl
c	40	20	0.7	20	3	US-09-357-071-44	Sequence 44, Appl
c	41	20	0.7	20	3	US-09-357-071-45	Sequence 45, Appl
c	42	20	0.7	20	3	US-09-357-071-46	Sequence 46, Appl
c	43	20	0.7	20	3	US-09-357-071-47	Sequence 47, Appl
	44	19.6	0.7	30	1	US-08-461-773-11	Sequence 11, Appl
c	45	18.2	0.6	24	3	US-09-118-408-28	Sequence 28, Appl

ALIGNMENTS

RESULT 1
US-09-357-071-4
; Sequence 4, Application US/09357071
; Patent No. 6043091
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowsert
; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE EXPRESSION
; FILE REFERENCE: RTS-0074
; CURRENT APPLICATION NUMBER: US/09/357,071
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 4
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Probe
US-09-357-071-4

Query Match 1.0%; Score 27; DB 3; Length 27;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 437 CTGTGATGAGGCCATTTACCAGCTTGG 463
||||||||||||||||||||||||||
Db 1 CTGTGATGAGGCCATTTACCAGCTTGG 27

RESULT 2
US-09-357-071-2
; Sequence 2, Application US/09357071
; Patent No. 6043091
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowsert
; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE EXPRESSION
; FILE REFERENCE: RTS-0074
; CURRENT APPLICATION NUMBER: US/09/357,071
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 2
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Primer
US-09-357-071-2

Query Match 0.7%; Score 21; DB 3; Length 21;

```
  Best Local Similarity   100.0%;  Pred. No. 1.2e+04;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        386 CATGGGCCGAACATTACAGAA 406
              ||||||||||||||||||||
Db          1 CATGGGCCGAACATTACAGAA 21


RESULT 3
US-09-357-071-3/c
; Sequence 3, Application US/09357071
; Patent No. 6043091
; GENERAL INFORMATION:
;  APPLICANT: Brett P. Monia
;  APPLICANT: Lex M. Cowsert
;  TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE EXPRESSION
;  FILE REFERENCE: RTS-0074
;  CURRENT APPLICATION NUMBER: US/09/357,071
;  CURRENT FILING DATE: 1999-07-19
;  NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 3
;   LENGTH: 21
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: PCR Primer
US-09-357-071-3

  Query Match             0.7%;  Score 21;  DB 3;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+04;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        505 GACTTGGCAATGGTGGTCTTG 525
              |||||||||||||||||||||
Db         21 GACTTGGCAATGGTGGTCTTG 1


RESULT 4
US-09-357-071-8/c
; Sequence 8, Application US/09357071
; Patent No. 6043091
; GENERAL INFORMATION:
;  APPLICANT: Brett P. Monia
;  APPLICANT: Lex M. Cowsert
;  TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE EXPRESSION
;  FILE REFERENCE: RTS-0074
;  CURRENT APPLICATION NUMBER: US/09/357,071
;  CURRENT FILING DATE: 1999-07-19
;  NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 8
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-357-071-8

  Query Match             0.7%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+04;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 CTCCTGGCGCGGCGGGGCGG 28
              ||||||||||||||||||||
Db         20 CTCCTGGCGCGGCGGGGCGG 1


RESULT 5
US-09-357-071-9/c
; Sequence 9, Application US/09357071
; Patent No. 6043091
; GENERAL INFORMATION:
;  APPLICANT: Brett P. Monia
;  APPLICANT: Lex M. Cowsert
;  TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE EXPRESSION
;  FILE REFERENCE: RTS-0074
;  CURRENT APPLICATION NUMBER: US/09/357,071
;  CURRENT FILING DATE: 1999-07-19
;  NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 9
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-357-071-9

  Query Match             0.7%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+04;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         71 CCAGCTCTCTGCGCAGCCCG 90
              ||||||||||||||||||||
Db         20 CCAGCTCTCTGCGCAGCCCG 1


RESULT 6
US-09-357-071-10/c
; Sequence 10, Application US/09357071
; Patent No. 6043091
; GENERAL INFORMATION:
;  APPLICANT: Brett P. Monia
;  APPLICANT: Lex M. Cowsert
;  TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE EXPRESSION
;  FILE REFERENCE: RTS-0074
;  CURRENT APPLICATION NUMBER: US/09/357,071
;  CURRENT FILING DATE: 1999-07-19
;  NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 10
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-357-071-10

  Query Match             0.7%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+04;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        109 CAGCCATGGGCGAACCGCTG 128
              ||||||||||||||||||||
Db         20 CAGCCATGGGCGAACCGCTG 1


RESULT 7
US-09-357-071-11/c
; Sequence 11, Application US/09357071
; Patent No. 6043091
; GENERAL INFORMATION:
;  APPLICANT: Brett P. Monia
;  APPLICANT: Lex M. Cowsert
;  TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE EXPRESSION
;  FILE REFERENCE: RTS-0074
;  CURRENT APPLICATION NUMBER: US/09/357,071
;  CURRENT FILING DATE: 1999-07-19
;  NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 11
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-357-071-11

  Query Match             0.7%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+04;
```

```
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        114 ATGGGCGAACCGCTGACAGA 133
              ||||||||||||||||||||
Db         20 ATGGGCGAACCGCTGACAGA 1


RESULT 8
US-09-357-071-12/c
; Sequence 12, Application US/09357071
; Patent No. 6043091
; GENERAL INFORMATION:
;  APPLICANT: Brett P. Monia
;  APPLICANT: Lex M. Cowsert
;  TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE EXPRESSION
;  FILE REFERENCE: RTS-0074
;  CURRENT APPLICATION NUMBER: US/09/357,071
;  CURRENT FILING DATE: 1999-07-19
;  NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 12
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-357-071-12

  Query Match             0.7%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+04;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        172 TGGGCGTGGAGAACGTGGCA 191
              ||||||||||||||||||||
Db         20 TGGGCGTGGAGAACGTGGCA 1


RESULT 9
US-09-357-071-13/c
; Sequence 13, Application US/09357071
; Patent No. 6043091
; GENERAL INFORMATION:
;  APPLICANT: Brett P. Monia
;  APPLICANT: Lex M. Cowsert
;  TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE EXPRESSION
;  FILE REFERENCE: RTS-0074
;  CURRENT APPLICATION NUMBER: US/09/357,071
;  CURRENT FILING DATE: 1999-07-19
;  NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 13
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-357-071-13

  Query Match             0.7%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+04;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        220 TGCACTTCACGCTGGTCAAG 239
              ||||||||||||||||||||
Db         20 TGCACTTCACGCTGGTCAAG 1


RESULT 10
US-09-357-071-14/c
; Sequence 14, Application US/09357071
; Patent No. 6043091
; GENERAL INFORMATION:
;  APPLICANT: Brett P. Monia
;  APPLICANT: Lex M. Cowsert
;  TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE EXPRESSION
;  FILE REFERENCE: RTS-0074
;  CURRENT APPLICATION NUMBER: US/09/357,071
;  CURRENT FILING DATE: 1999-07-19
;  NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 14
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-357-071-14

  Query Match             0.7%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+04;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        260 CCGCGACTACTACTTCGCGC 279
              ||||||||||||||||||||
Db         20 CCGCGACTACTACTTCGCGC 1


RESULT 11
US-09-357-071-15/c
; Sequence 15, Application US/09357071
; Patent No. 6043091
; GENERAL INFORMATION:
;  APPLICANT: Brett P. Monia
;  APPLICANT: Lex M. Cowsert
;  TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE EXPRESSION
;  FILE REFERENCE: RTS-0074
;  CURRENT APPLICATION NUMBER: US/09/357,071
;  CURRENT FILING DATE: 1999-07-19
;  NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 15
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-357-071-15

  Query Match             0.7%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+04;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        299 CCACCTGGTGGGGCGCTGGA 318
              ||||||||||||||||||||
Db         20 CCACCTGGTGGGGCGCTGGA 1


RESULT 12
US-09-357-071-16/c
; Sequence 16, Application US/09357071
; Patent No. 6043091
; GENERAL INFORMATION:
;  APPLICANT: Brett P. Monia
;  APPLICANT: Lex M. Cowsert
;  TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE EXPRESSION
;  FILE REFERENCE: RTS-0074
;  CURRENT APPLICATION NUMBER: US/09/357,071
;  CURRENT FILING DATE: 1999-07-19
;  NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 16
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-357-071-16

  Query Match             0.7%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+04;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy        372 TCTCTGGAATTTTACATGGG 391
              ||||||||||||||||||||
Db         20 TCTCTGGAATTTTACATGGG 1


RESULT 13
US-09-357-071-17/c
; Sequence 17, Application US/09357071
; Patent No. 6043091
; GENERAL INFORMATION:
;  APPLICANT: Brett P. Monia
;  APPLICANT: Lex M. Cowsert
;  TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE EXPRESSION
;  FILE REFERENCE: RTS-0074
;  CURRENT APPLICATION NUMBER: US/09/357,071
;  CURRENT FILING DATE: 1999-07-19
;  NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 17
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-357-071-17

  Query Match             0.7%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+04;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        415 TCAACCTCGGTCTGCAAAAT 434
              ||||||||||||||||||||
Db         20 TCAACCTCGGTCTGCAAAAT 1


RESULT 14
US-09-357-071-18/c
; Sequence 18, Application US/09357071
; Patent No. 6043091
; GENERAL INFORMATION:
;  APPLICANT: Brett P. Monia
;  APPLICANT: Lex M. Cowsert
;  TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE EXPRESSION
;  FILE REFERENCE: RTS-0074
;  CURRENT APPLICATION NUMBER: US/09/357,071
;  CURRENT FILING DATE: 1999-07-19
;  NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 18
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-357-071-18

  Query Match             0.7%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+04;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        460 TTGGATTGGATATAGAAGAG 479
              ||||||||||||||||||||
Db         20 TTGGATTGGATATAGAAGAG 1


RESULT 15
US-09-357-071-19/c
; Sequence 19, Application US/09357071
; Patent No. 6043091
; GENERAL INFORMATION:
;  APPLICANT: Brett P. Monia
;  APPLICANT: Lex M. Cowsert
;  TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE EXPRESSION
;  FILE REFERENCE: RTS-0074
;  CURRENT APPLICATION NUMBER: US/09/357,071
;  CURRENT FILING DATE: 1999-07-19
;  NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 19
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-357-071-19

  Query Match             0.7%;  Score 20;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+04;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        523 TTGGGAGACTTGCTGCCTGC 542
              ||||||||||||||||||||
Db         20 TTGGGAGACTTGCTGCCTGC 1


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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

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(without alignments)
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Title: US-10-019-470-1
Perfect score: 2828
Sequence: 1 gttgaaagctcctggcgcgg.....aaagtgtcaatttccaagga 2828

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3304383 seqs, 2515761380 residues

Total number of hits satisfying chosen parameters: 1414684

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
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9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq2:*
14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	27	1.0	27	15	US-10-114-544-4	Sequence 4, Appli
	2	21	0.7	21	15	US-10-114-544-2	Sequence 2, Appli
c	3	21	0.7	21	15	US-10-114-544-3	Sequence 3, Appli
c	4	20	0.7	20	15	US-10-114-544-8	Sequence 8, Appli
c	5	20	0.7	20	15	US-10-114-544-9	Sequence 9, Appli
c	6	20	0.7	20	15	US-10-114-544-10	Sequence 10, Appl
c	7	20	0.7	20	15	US-10-114-544-11	Sequence 11, Appl
c	8	20	0.7	20	15	US-10-114-544-12	Sequence 12, Appl
c	9	20	0.7	20	15	US-10-114-544-13	Sequence 13, Appl
c	10	20	0.7	20	15	US-10-114-544-14	Sequence 14, Appl
c	11	20	0.7	20	15	US-10-114-544-15	Sequence 15, Appl
c	12	20	0.7	20	15	US-10-114-544-16	Sequence 16, Appl
c	13	20	0.7	20	15	US-10-114-544-17	Sequence 17, Appl
c	14	20	0.7	20	15	US-10-114-544-18	Sequence 18, Appl
c	15	20	0.7	20	15	US-10-114-544-19	Sequence 19, Appl
c	16	20	0.7	20	15	US-10-114-544-20	Sequence 20, Appl
c	17	20	0.7	20	15	US-10-114-544-21	Sequence 21, Appl
c	18	20	0.7	20	15	US-10-114-544-22	Sequence 22, Appl
c	19	20	0.7	20	15	US-10-114-544-23	Sequence 23, Appl
c	20	20	0.7	20	15	US-10-114-544-24	Sequence 24, Appl
c	21	20	0.7	20	15	US-10-114-544-25	Sequence 25, Appl
c	22	20	0.7	20	15	US-10-114-544-26	Sequence 26, Appl
c	23	20	0.7	20	15	US-10-114-544-27	Sequence 27, Appl
c	24	20	0.7	20	15	US-10-114-544-28	Sequence 28, Appl
c	25	20	0.7	20	15	US-10-114-544-29	Sequence 29, Appl
c	26	20	0.7	20	15	US-10-114-544-30	Sequence 30, Appl
c	27	20	0.7	20	15	US-10-114-544-31	Sequence 31, Appl
c	28	20	0.7	20	15	US-10-114-544-32	Sequence 32, Appl
c	29	20	0.7	20	15	US-10-114-544-33	Sequence 33, Appl
c	30	20	0.7	20	15	US-10-114-544-34	Sequence 34, Appl
c	31	20	0.7	20	15	US-10-114-544-35	Sequence 35, Appl
c	32	20	0.7	20	15	US-10-114-544-36	Sequence 36, Appl
c	33	20	0.7	20	15	US-10-114-544-37	Sequence 37, Appl
c	34	20	0.7	20	15	US-10-114-544-38	Sequence 38, Appl
c	35	20	0.7	20	15	US-10-114-544-39	Sequence 39, Appl
c	36	20	0.7	20	15	US-10-114-544-40	Sequence 40, Appl
c	37	20	0.7	20	15	US-10-114-544-41	Sequence 41, Appl
c	38	20	0.7	20	15	US-10-114-544-42	Sequence 42, Appl
c	39	20	0.7	20	15	US-10-114-544-43	Sequence 43, Appl
c	40	20	0.7	20	15	US-10-114-544-44	Sequence 44, Appl
c	41	20	0.7	20	15	US-10-114-544-45	Sequence 45, Appl
c	42	20	0.7	20	15	US-10-114-544-46	Sequence 46, Appl
c	43	20	0.7	20	15	US-10-114-544-47	Sequence 47, Appl
c	44	19.6	0.7	27	15	US-10-023-586B-5	Sequence 5, Appli
c	45	19.6	0.7	27	17	US-10-763-972-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-10-114-544-4
; Sequence 4, Application US/10114544
; Publication No. US20030166592A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowsert
; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: RTSP-0240
; CURRENT APPLICATION NUMBER: US/10/114,544
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 10/019,470
; PRIOR FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: US 09/357,071
; PRIOR FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 4
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Probe
US-10-114-544-4

Query Match 1.0%; Score 27; DB 15; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 437 CTGTGATGAGGCCATTTACCAGCTTGG 463
||||||||||||||||||||||||||||
Db 1 CTGTGATGAGGCCATTTACCAGCTTGG 27

RESULT 2
US-10-114-544-2
; Sequence 2, Application US/10114544

; Publication No. US20030166592A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowsert
; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: RTSP-0240
; CURRENT APPLICATION NUMBER: US/10/114,544
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 10/019,470
; PRIOR FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: US 09/357,071
; PRIOR FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 2
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Primer
US-10-114-544-2

Query Match 0.7%; Score 21; DB 15; Length 21;
Best Local Similarity 100.0%; Pred. No. 6.1e+04;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 386 CATGGGCCGAACATTACAGAA 406
||||||||||||||||||||
Db 1 CATGGGCCGAACATTACAGAA 21

RESULT 3
US-10-114-544-3/c
; Sequence 3, Application US/10114544
; Publication No. US20030166592A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowsert
; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: RTSP-0240
; CURRENT APPLICATION NUMBER: US/10/114,544
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 10/019,470
; PRIOR FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: US 09/357,071
; PRIOR FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 3
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Primer
US-10-114-544-3

Query Match 0.7%; Score 21; DB 15; Length 21;
Best Local Similarity 100.0%; Pred. No. 6.1e+04;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 505 GACTTGGCAATGGTGGTCTTG 525
||||||||||||||||||||
Db 21 GACTTGGCAATGGTGGTCTTG 1

RESULT 4
US-10-114-544-8/c
; Sequence 8, Application US/10114544
; Publication No. US20030166592A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowsert
; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: RTSP-0240
; CURRENT APPLICATION NUMBER: US/10/114,544
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 10/019,470
; PRIOR FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: US 09/357,071
; PRIOR FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 8
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-114-544-8

Query Match 0.7%; Score 20; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CTCCTGGCGCGGCGGGGCGG 28
||||||||||||||||||||
Db 20 CTCCTGGCGCGGCGGGGCGG 1

RESULT 5
US-10-114-544-9/c
; Sequence 9, Application US/10114544
; Publication No. US20030166592A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowsert
; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: RTSP-0240
; CURRENT APPLICATION NUMBER: US/10/114,544
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 10/019,470
; PRIOR FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: US 09/357,071
; PRIOR FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 9
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-114-544-9

Query Match 0.7%; Score 20; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 71 CCAGCTCTCTGCGCAGCCCG 90
||||||||||||||||||||
Db 20 CCAGCTCTCTGCGCAGCCCG 1

RESULT 6
US-10-114-544-10/c
; Sequence 10, Application US/10114544
; Publication No. US20030166592A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowsert
; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: RTSP-0240
; CURRENT APPLICATION NUMBER: US/10/114,544
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 10/019,470

```
;  PRIOR FILING DATE: 2001-12-28
;  PRIOR APPLICATION NUMBER: US 09/357,071
;  PRIOR FILING DATE: 1999-07-19
;  NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 10
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-114-544-10

  Query Match             0.7%;  Score 20;  DB 15;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+05;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        109 CAGCCATGGGCGAACCGCTG 128
              ||||||||||||||||||||
Db         20 CAGCCATGGGCGAACCGCTG 1


RESULT 7
US-10-114-544-11/c
; Sequence 11, Application US/10114544
; Publication No. US20030166592A1
; GENERAL INFORMATION:
;  APPLICANT: Brett P. Monia
;  APPLICANT:  Lex M. Cowsert
;  TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE
;  TITLE OF INVENTION:  EXPRESSION
;  FILE REFERENCE: RTSP-0240
;  CURRENT APPLICATION NUMBER: US/10/114,544
;  CURRENT FILING DATE:  2002-04-01
;  PRIOR APPLICATION NUMBER: 10/019,470
;  PRIOR FILING DATE: 2001-12-28
;  PRIOR APPLICATION NUMBER: US 09/357,071
;  PRIOR FILING DATE: 1999-07-19
;  NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 11
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-114-544-11

  Query Match             0.7%;  Score 20;  DB 15;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+05;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        114 ATGGGCGAACCGCTGACAGA 133
              ||||||||||||||||||||
Db         20 ATGGGCGAACCGCTGACAGA 1


RESULT 8
US-10-114-544-12/c
; Sequence 12, Application US/10114544
; Publication No. US20030166592A1
; GENERAL INFORMATION:
;  APPLICANT: Brett P. Monia
;  APPLICANT:  Lex M. Cowsert
;  TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE
;  TITLE OF INVENTION:  EXPRESSION
;  FILE REFERENCE: RTSP-0240
;  CURRENT APPLICATION NUMBER: US/10/114,544
;  CURRENT FILING DATE:  2002-04-01
;  PRIOR APPLICATION NUMBER: 10/019,470
;  PRIOR FILING DATE: 2001-12-28
;  PRIOR APPLICATION NUMBER: US 09/357,071
;  PRIOR FILING DATE: 1999-07-19
;  NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 12
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-114-544-12

  Query Match             0.7%;  Score 20;  DB 15;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+05;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        172 TGGGCGTGGAGAACGTGGCA 191
              ||||||||||||||||||||
Db         20 TGGGCGTGGAGAACGTGGCA 1


RESULT 9
US-10-114-544-13/c
; Sequence 13, Application US/10114544
; Publication No. US20030166592A1
; GENERAL INFORMATION:
;  APPLICANT: Brett P. Monia
;  APPLICANT:  Lex M. Cowsert
;  TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE
;  TITLE OF INVENTION:  EXPRESSION
;  FILE REFERENCE: RTSP-0240
;  CURRENT APPLICATION NUMBER: US/10/114,544
;  CURRENT FILING DATE:  2002-04-01
;  PRIOR APPLICATION NUMBER: 10/019,470
;  PRIOR FILING DATE: 2001-12-28
;  PRIOR APPLICATION NUMBER: US 09/357,071
;  PRIOR FILING DATE: 1999-07-19
;  NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 13
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-114-544-13

  Query Match             0.7%;  Score 20;  DB 15;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+05;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        220 TGCACTTCACGCTGGTCAAG 239
              ||||||||||||||||||||
Db         20 TGCACTTCACGCTGGTCAAG 1


RESULT 10
US-10-114-544-14/c
; Sequence 14, Application US/10114544
; Publication No. US20030166592A1
; GENERAL INFORMATION:
;  APPLICANT: Brett P. Monia
;  APPLICANT:  Lex M. Cowsert
;  TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE
;  TITLE OF INVENTION:  EXPRESSION
;  FILE REFERENCE: RTSP-0240
;  CURRENT APPLICATION NUMBER: US/10/114,544
;  CURRENT FILING DATE:  2002-04-01
;  PRIOR APPLICATION NUMBER: 10/019,470
;  PRIOR FILING DATE: 2001-12-28
;  PRIOR APPLICATION NUMBER: US 09/357,071
;  PRIOR FILING DATE: 1999-07-19
;  NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 14
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
```

US-10-114-544-14

Query Match 0.7%; Score 20; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        260 CCGCGACTACTACTTCGCGC 279
              ||||||||||||||||||||
Db         20 CCGCGACTACTACTTCGCGC 1
```

RESULT 11
US-10-114-544-15/c
; Sequence 15, Application US/10114544
; Publication No. US20030166592A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowsert
; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: RTSP-0240
; CURRENT APPLICATION NUMBER: US/10/114,544
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 10/019,470
; PRIOR FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: US 09/357,071
; PRIOR FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 15
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-114-544-15

Query Match 0.7%; Score 20; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        299 CCACCTGGTGGGGCGCTGGA 318
              ||||||||||||||||||||
Db         20 CCACCTGGTGGGGCGCTGGA 1
```

RESULT 12
US-10-114-544-16/c
; Sequence 16, Application US/10114544
; Publication No. US20030166592A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowsert
; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: RTSP-0240
; CURRENT APPLICATION NUMBER: US/10/114,544
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 10/019,470
; PRIOR FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: US 09/357,071
; PRIOR FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 16
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-114-544-16

Query Match 0.7%; Score 20; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        372 TCTCTGGAATTTTACATGGG 391
              ||||||||||||||||||||
Db         20 TCTCTGGAATTTTACATGGG 1
```

RESULT 13
US-10-114-544-17/c
; Sequence 17, Application US/10114544
; Publication No. US20030166592A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowsert
; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: RTSP-0240
; CURRENT APPLICATION NUMBER: US/10/114,544
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 10/019,470
; PRIOR FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: US 09/357,071
; PRIOR FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 17
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-114-544-17

Query Match 0.7%; Score 20; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        415 TCAACCTCGGTCTGCAAAAT 434
              ||||||||||||||||||||
Db         20 TCAACCTCGGTCTGCAAAAT 1
```

RESULT 14
US-10-114-544-18/c
; Sequence 18, Application US/10114544
; Publication No. US20030166592A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowsert
; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: RTSP-0240
; CURRENT APPLICATION NUMBER: US/10/114,544
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 10/019,470
; PRIOR FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: US 09/357,071
; PRIOR FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 18
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-114-544-18

Query Match 0.7%; Score 20; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        460 TTGGATTGGATATAGAAGAG 479
              ||||||||||||||||||||
Db         20 TTGGATTGGATATAGAAGAG 1
```

```
RESULT 15
US-10-114-544-19/c
; Sequence 19, Application US/10114544
; Publication No. US20030166592A1
; GENERAL INFORMATION:
;  APPLICANT: Brett P. Monia
;  APPLICANT:  Lex M. Cowsert
;  TITLE OF INVENTION: ANTISENSE MODULATION OF LIVER GLYCOGEN PHOSPHORYLASE
;  TITLE OF INVENTION:  EXPRESSION
;  FILE REFERENCE: RTSP-0240
;  CURRENT APPLICATION NUMBER: US/10/114,544
;  CURRENT FILING DATE:  2002-04-01
;  PRIOR APPLICATION NUMBER: 10/019,470
;  PRIOR FILING DATE: 2001-12-28
;  PRIOR APPLICATION NUMBER: US 09/357,071
;  PRIOR FILING DATE: 1999-07-19
;  NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 19
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-114-544-19

  Query Match             0.7%;  Score 20;  DB 15;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+05;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        523 TTGGGAGACTTGCTGCCTGC 542
              ||||||||||||||||||||
Db         20 TTGGGAGACTTGCTGCCTGC 1


Search completed: September 15, 2004, 13:01:36
Job time : 1266 secs
```

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: September 15, 2004, 06:43:50 ; Search time 7035 Seconds
(without alignments)
12004.299 Million cell updates/sec

Title: US-10-019-470-1
Perfect score: 2828
Sequence: 1 gttgaaagctcctggcgcgg.....aaagtgtcaatttccaagga 2828

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 38748

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		17.2	0.6	28	28	AZ782046	AZ782046 2M0021N19
2	c	17.2	0.6	29	28	AZ514403	AZ514403 1M0361K06
3		16.6	0.6	30	28	AZ990068	AZ990068 2M0273G07
4	c	16.4	0.6	29	28	AZ331559	AZ331559 1M0059L06
5	c	16.2	0.6	30	14	CF305882	CF305882 HDA1--02-
6	c	16.2	0.6	30	28	CC458485	CC458485 SALK_1192
7		16	0.6	26	14	D11539	D11539 HUM0C12B04
8	c	16	0.6	26	28	BH908631	BH908631 SALK_0497
9	c	16	0.6	27	29	TA128C06P	AL464342 T. brucei
10		16	0.6	28	28	AZ760461	AZ760461 1M0554C13
11	c	16	0.6	29	28	AZ323903	AZ323903 1M0045A07
12		16	0.6	29	28	AZ658502	AZ658502 1M0535M12
13		16	0.6	30	28	AZ458346	AZ458346 1M0262P13
14		15.8	0.6	21	9	AU264676	AU264676 AU264676
15	c	15.8	0.6	23	28	AZ433969	AZ433969 1M0220E07
16		15.8	0.6	27	14	D25863	D25863 HUMGS04241
17	c	15.8	0.6	28	9	AI826975	AI826975 wk55a12.x
18		15.8	0.6	28	28	AZ799395	AZ799395 2M0056N16
19		15.8	0.6	29	28	AZ475726	AZ475726 1M0294F02
20	c	15.8	0.6	29	28	BZ764283	BZ764283 SALK_1242
21	c	15.8	0.6	30	14	T63438	T63438 yc07e02.r1
22	c	15.8	0.6	30	28	AZ433900	AZ433900 1M0220F03
23		15.8	0.6	30	28	BH857708	BH857708 SALK_0160
24		15.8	0.6	30	29	AL937504	AL937504 Arabidops
25	c	15.6	0.6	25	29	TA232H10P	AL481055 T. brucei
26	c	15.6	0.6	26	28	AZ832213	AZ832213 2M0112C03
27		15.6	0.6	28	9	AI815651	AI815651 au49b06.y
28	c	15.6	0.6	28	28	AZ458545	AZ458545 1M0262B15
29		15.6	0.6	29	29	TA18B08P	AL451961 T. brucei
30		15.4	0.5	25	9	AI808531	AI808531 wf95e12.x
31	c	15.4	0.5	25	13	C21101	C21101 HUMGS000262
32		15.4	0.5	25	13	C21203	C21203 HUMGS000223
33		15.4	0.5	26	28	AZ579502	AZ579502 1M0367D12
34	c	15.4	0.5	26	29	CG712612	CG712612 1119027G1
35		15.4	0.5	28	28	AZ648296	AZ648296 1M0517E15
36		15.4	0.5	30	28	AZ475143	AZ475143 1M0293G22
37	c	15.2	0.5	21	9	AB088507	AB088507 AB088507
38	c	15.2	0.5	23	28	CC455757	CC455757 SALK_0864
39	c	15.2	0.5	26	9	AU266262	AU266262 AU266262
40		15.2	0.5	27	9	AU264164	AU264164 AU264164
41	c	15.2	0.5	28	9	AA027602	AA027602 mi12d08.r
42		15.2	0.5	28	9	AI687937	AI687937 tp99d01.x
43		15.2	0.5	28	28	AZ466667	AZ466667 1M0277G06
44	c	15.2	0.5	29	9	AU014027	AU014027 AU014027
45		15.2	0.5	29	28	AZ587944	AZ587944 1M0395O23

ALIGNMENTS

RESULT 1
AZ782046
LOCUS AZ782046 28 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M0021N19R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0021N19 R, genomic survey sequence.
ACCESSION AZ782046
VERSION AZ782046.1 GI:12915346
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 28)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

```
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0021  row: N  column: 19
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 28.
FEATURES              Location/Qualifiers
     source           1. .28
                      /organism="Mus musculus"
                      /mol_type="genomic DNA"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="UUGC2M0021N19"
                      /sex="Male"
                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                      /clone_lib="Mouse 10kb plasmid UUGC1M library"
                      /note="Vector: PWD42nv; Purified genomic DNA from M.
                      musculus C57BL/6J (male) was obtained  from the Jackson
                      Laboratory Mouse DNA Resource
                      (http://www.jax.org/resources/documents/dnares/). The DNA
                      was hydrodynamically sheared by repeated passage through a
                      0.005 inch orifice at constant velocity. The sheared DNA
                      was blunt end-repaired with T4 DNA polymerase and T4
                      polynucleotide kinase. Adaptor oligonucleotides were
                      ligated to the blunt ends in high  molar excess. The
                      adaptored DNA was purified and size-selected for a 9.5 to
                      10.5 kb range using preparative agarose gel
                      electrophoresis. Vector DNA was prepared from a derivative
                      of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                      inducible derivative of plasmid R1. The vector was ligated
                      with adaptors complementary to the insert adaptors and
                      purified. The sheared, adaptored mouse DNA was annealed to
                      adaptored vector DNA, and transformed into
                      chemically-competent E. coli XL10-Gold (Stratagene) cells
                      and selected for ampicillin resistance."
ORIGIN

  Query Match             0.6%;  Score 17.2;  DB 28;  Length 28;
  Best Local Similarity   86.4%;  Pred. No. 1.9e+07;
  Matches   19;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1594 TACTCTGCAACCCAGGACTTGC 1615
              ||||||  |||||||||||  ||
Db          2 TACTCTCTAACCCAGGACTGGC 23


RESULT 2
AZ514403/c
LOCUS       AZ514403                  29 bp    DNA     linear   GSS 05-OCT-2000
DEFINITION  1M0361K06F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0361K06 F, genomic survey sequence.
ACCESSION   AZ514403
VERSION     AZ514403.1  GI:10695719
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
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            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0361  row: K  column: 06
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 29.
FEATURES              Location/Qualifiers
     source           1. .29
                      /organism="Mus musculus"
                      /mol_type="genomic DNA"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="UUGC1M0361K06"
                      /sex="Male"
                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                      /clone_lib="Mouse 10kb plasmid UUGC1M library"
                      /note="Vector: PWD42nv; Purified genomic DNA from M.
                      musculus C57BL/6J (male) was obtained  from the Jackson
                      Laboratory Mouse DNA Resource
                      (http://www.jax.org/resources/documents/dnares/). The DNA
                      was hydrodynamically sheared by repeated passage through a
                      0.005 inch orifice at constant velocity. The sheared DNA
                      was blunt end-repaired with T4 DNA polymerase and T4
                      polynucleotide kinase. Adaptor oligonucleotides were
                      ligated to the blunt ends in high  molar excess. The
                      adaptored DNA was purified and size-selected for a 9.5 to
                      10.5 kb range using preparative agarose gel
                      electrophoresis. Vector DNA was prepared from a derivative
                      of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                      inducible derivative of plasmid R1. The vector was ligated
                      with adaptors complementary to the insert adaptors and
                      purified. The sheared, adaptored mouse DNA was annealed to
                      adaptored vector DNA, and transformed into
                      chemically-competent E. coli XL10-Gold (Stratagene) cells
                      and selected for ampicillin resistance."
ORIGIN

  Query Match             0.6%;  Score 17.2;  DB 28;  Length 29;
  Best Local Similarity   86.4%;  Pred. No. 1.9e+07;
  Matches   19;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        466 TGGATATAGAAGAGTTAGAAGA 487
              || |||||||||| || ||||
Db         29 TGAATATAGAAGAGATATAAGA 8


RESULT 3
AZ990068
LOCUS       AZ990068                  30 bp    DNA     linear   GSS 27-APR-2001
DEFINITION  2M0273G07R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
            clone UUGC2M0273G07 R, genomic survey sequence.
ACCESSION   AZ990068
VERSION     AZ990068.1  GI:13861295
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
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            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0273  row: G  column: 07
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 30.
FEATURES              Location/Qualifiers
     source           1. .30
                      /organism="Mus musculus"
                      /mol_type="genomic DNA"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="UUGC2M0273G07"
                      /sex="Female"
                      /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
                      /clone_lib="Mouse 10kb plasmid UUGC2M library"
                      /note="Vector: PWD42nv; Purified genomic DNA from M.
                      musculus C57BL/6J (female) was obtained  from the Jackson
                      Laboratory Mouse DNA Resource
                      (http://www.jax.org/resources/documents/dnares/). The DNA
                      was hydrodynamically sheared by repeated passage through a
                      0.005 inch orifice at constant velocity. The sheared DNA
                      was blunt end-repaired with T4 DNA polymerase and T4
                      polynucleotide kinase. Adaptor oligonucleotides were
                      ligated to the blunt ends in high  molar excess. The
                      adaptored DNA was purified and size-selected for a 9.5 to
                      10.5 kb range using preparative agarose gel
                      electrophoresis. Vector DNA was prepared from a derivative
                      of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                      inducible derivative of plasmid R1. The vector was ligated
                      with adaptors complementary to the insert adaptors and
                      purified. The sheared, adaptored mouse DNA was annealed to
                      adaptored vector DNA, and transformed into
                      chemically-competent E. coli XL10-Gold (Stratagene) cells
                      and selected for ampicillin resistance."
ORIGIN

  Query Match             0.6%;  Score 16.6;  DB 28;  Length 30;
  Best Local Similarity   82.6%;  Pred. No. 2.7e+07;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        241 ACCGCAACGTGGCCACCACCCGC 263
              |||| ||||||| ||| |||| |
Db          8 ACCGGAACGTGGACACGACCCAC 30


RESULT 4
AZ331559/c
LOCUS       AZ331559                 29 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0059L06R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0059L06 R, genomic survey sequence.
ACCESSION   AZ331559
VERSION     AZ331559.1  GI:10394372
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0059  row: L  column: 06
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 29.
FEATURES              Location/Qualifiers
     source           1. .29
                      /organism="Mus musculus"
                      /mol_type="genomic DNA"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="UUGC1M0059L06"
                      /sex="Male"
                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                      /clone_lib="Mouse 10kb plasmid UUGC1M library"
                      /note="Vector: PWD42nv; Purified genomic DNA from M.
                      musculus C57BL/6J (male) was obtained  from the Jackson
                      Laboratory Mouse DNA Resource
                      (http://www.jax.org/resources/documents/dnares/). The DNA
                      was hydrodynamically sheared by repeated passage through a
                      0.005 inch orifice at constant velocity. The sheared DNA
                      was blunt end-repaired with T4 DNA polymerase and T4
                      polynucleotide kinase. Adaptor oligonucleotides were
                      ligated to the blunt ends in high  molar excess. The
                      adaptored DNA was purified and size-selected for a 9.5 to
                      10.5 kb range using preparative agarose gel
                      electrophoresis. Vector DNA was prepared from a derivative
                      of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                      inducible derivative of plasmid R1. The vector was ligated
                      with adaptors complementary to the insert adaptors and
                      purified. The sheared, adaptored mouse DNA was annealed to
                      adaptored vector DNA, and transformed into
                      chemically-competent E. coli XL10-Gold (Stratagene) cells
                      and selected for ampicillin resistance."
ORIGIN

  Query Match             0.6%;  Score 16.4;  DB 28;  Length 29;
  Best Local Similarity   76.9%;  Pred. No. 3e+07;
  Matches   20;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy        726 GGAAAAGTAGAACACACCAACACCGG 751
              ||||| |  |||||| || |||| ||
Db         27 GGAAATGATGAACACCCCCACACAGG 2


RESULT 5
CF305882/c
LOCUS       CF305882                 30 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HDA1--02-A08.g1 OsHDAC1-overexpressing transgenic rice lambda phage
            cDNA library I (HDA1) Oryza sativa cDNA clone HDA1--02-A08, mRNA
            sequence.
ACCESSION   CF305882
VERSION     CF305882.1  GI:33677643
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES              Location/Qualifiers
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     source          1. .30
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="HDA1--02-A08"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli SOLR"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice lambda
                     phage cDNA library I (HDA1)"
                     /note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
                     XhoI; Callus was treated with ABA(20um) for 1hour. cDNA
                     was inserted into lambda Uni-ZAP XR vector at 5' end with
                     EcoRI and 3' end with XhoI site. mRNA was derived from
                     rice Histone Deacetylase overexpression line."
ORIGIN

  Query Match             0.6%;  Score 16.2;  DB 14;  Length 30;
  Best Local Similarity   72.4%;  Pred. No. 3.3e+07;
  Matches   21;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy        289 CGGTGCGGGACCACCTGGTGGGGCGCTGG 317
              | | | | |  | |||| ||||||||||
Db         30 CTGCGGGTGTGCTCCTGTTGGGGCGCTGG 2


RESULT 6
CC458485/c
LOCUS       CC458485                 30 bp    DNA     linear   GSS 30-MAY-2003
DEFINITION  SALK_119217.40.80.x Arabidopsis thaliana TDNA insertion lines
            Arabidopsis thaliana genomic clone SALK_119217.40.80.x, genomic
            survey sequence.
ACCESSION   CC458485
VERSION     CC458485.1  GI:31222685
KEYWORDS    GSS.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
            Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
            Shinn,P., Zimmerman,J. and Ecker,J.R.
  TITLE     A Sequence-Indexed Library of Insertion Mutations in the
            Arabidopsis Genome
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Joseph R. Ecker
            Salk Institute Genomic Analysis Laboratory (SIGnAL)
            The Salk Institute for Biological Studies
            10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
            Tel: 858 453 4100 x1752
            Fax: 858 558 6379
            Email: ecker@salk.edu
            This is single pass sequence recovered from the left border of
            TDNA. This sequence lies within an annotated intron of At3g55380.
            Class: TDNA tagged.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /strain="Columbia 0"
                     /db_xref="taxon:3702"
                     /clone="SALK_119217.40.80.x"
                     /clone_lib="Arabidopsis thaliana TDNA insertion lines"
                     /note="PCR was performed on Arabidopsis thaliana lines
                     each of which contains  one or more TDNA insertion
                     elements. The resultant fragment for each  line was
                     directly sequenced to determine the genomic sequence at
                     the  site of insertion. Details of the protocols used can
                     be found at  http://signal.salk.edu/tdna_protocols.html"
ORIGIN

  Query Match             0.6%;  Score 16.2;  DB 28;  Length 30;
  Best Local Similarity   72.4%;  Pred. No. 3.3e+07;
  Matches   21;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy       2616 ATTTCTCTATCCAATGAATCTAACAAAGT 2644
              | |  | |||||||||| |  | ||||||
Db         29 AATGTTTTATCCAATGAGTGGAGCAAAGT 1


RESULT 7
D11539
LOCUS       D11539                   26 bp    mRNA    linear   EST 21-JUL-1994
DEFINITION  HUM0C12B04 Liver HepG2 cell line. Homo sapiens cDNA clone c12b04
            3', mRNA sequence.
ACCESSION   D11539
VERSION     D11539.1  GI:511920
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Okubo,K., Hori,N., Matoba,R., Niiyama,T., Fukushima,A., Kojima,Y.
            and Matsubara,K.
  TITLE     Large scale cDNA sequencing for analysis of quantitative and
            qualitative aspects of gene expression
  JOURNAL   Nat. Genet. 2, 173-179 (1992)
  MEDLINE   94258199
   PUBMED   1345164
COMMENT     Contact: Kousaku Okubo, Naohiro Hori, Ryo Matoba, Toshiyuki
            Niiyama, Atsushi Fukushima, Yuko Kojima & Kenichi Matsubara
            Institute for Molecular and Cellular Biology
            Osaka University
            1-3 Yamada-oka,Suita,Osaka 565,Japan.
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="GDB:D0S8041E"
                     /db_xref="taxon:9606"
                     /clone="c12b04"
                     /lab_host="E.coli"
                     /clone_lib="Liver HepG2 cell line."
                     /note="3'-directed regional cDNA library. Cleaved by MboI
                     and transformed into E.coli."
ORIGIN

  Query Match             0.6%;  Score 16;  DB 14;  Length 26;
  Best Local Similarity   79.2%;  Pred. No. 3.5e+07;
  Matches   19;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2633 ATCTAACAAAGTCAATGGAAATTG 2656
              ||| || |||||  ||| ||||||
Db          2 ATCAAAGAAAGTTTATGAAAATTG 25


RESULT 8
BH908631/c
LOCUS       BH908631                 26 bp    DNA     linear   GSS 04-SEP-2002
DEFINITION  SALK_049758.30.10.x Arabidopsis thaliana TDNA insertion lines
            Arabidopsis thaliana genomic clone SALK_049758.30.10.x, genomic
            survey sequence.
ACCESSION   BH908631
VERSION     BH908631.1  GI:22721564
KEYWORDS    GSS.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
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            Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
            Shinn,P., Zimmerman,J. and Ecker,J.R.
  TITLE     A Sequence-Indexed Library of Insertion Mutations in the
            Arabidopsis Genome
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Joseph R. Ecker
            Salk Institute Genomic Analysis Laboratory (SIGnAL)
            The Salk Institute for Biological Studies
            10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
            Tel: 858 453 4100 x1752
            Fax: 858 558 6379
            Email: ecker@salk.edu
            This is single pass sequence recovered from the left border of
            TDNA.
            Class: TDNA tagged.
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /strain="Columbia 0"
                     /db_xref="taxon:3702"
                     /clone="SALK_049758.30.10.x"
                     /clone_lib="Arabidopsis thaliana TDNA insertion lines"
                     /note="PCR was performed on Arabidopsis thaliana lines
                     each of which contains  one or more TDNA insertion
                     elements. The resultant fragment for each  line was
                     directly sequenced to determine the genomic sequence at
                     the  site of insertion. Details of the protocols used can
                     be found at  http://signal.salk.edu/tdna_protocols.html"
ORIGIN

  Query Match              0.6%;  Score 16;  DB 28;  Length 26;
  Best Local Similarity   79.2%;  Pred. No. 3.5e+07;
  Matches   19;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2623 TATCCAATGAATCTAACAAAGTCA 2646
                ||  |||| |||||||| || |||
Db         25 TAATCAATCAATCTAACCAAATCA 2


RESULT 9
TA128C06P/c
LOCUS       TA128C06P                 27 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  T. brucei sheared genomic DNA clone 128c06, forward sequence,
            genomic survey sequence.
ACCESSION   AL464342
VERSION     AL464342.1  GI:11834605
KEYWORDS    GSS.
SOURCE      Trypanosoma brucei
  ORGANISM  Trypanosoma brucei
            Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
            Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
            Melville,S.E., Rajandream,M.A. and Barrell,B.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
            project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
            Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
            nh1@sanger.ac.uk
COMMENT     Constructed at the Institute for Genomic Research (TIGR),
            Rockville, MD. Genomic DNA isolated from a cloned population of
            Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
            to give a tight size distribution (
            4 kb).  The v + i method used for the library construction is
            described in detail in Smith, H. and Venter, J.C. (Making small
            insert libraries for whole genome shotgun sequencing projects.  In
            Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
            Barrell, Oxford University Press, 1999).
            Email: nelsayed@tigr.org
            Details of T. brucei sequencing at the Sanger Centre are available
            at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="Trypanosoma brucei"
                     /mol_type="genomic DNA"
                     /strain="TREU927"
                     /db_xref="taxon:5691"
                     /clone="128c06"
ORIGIN

  Query Match              0.6%;  Score 16;  DB 29;  Length 27;
  Best Local Similarity   79.2%;  Pred. No. 3.5e+07;
  Matches   19;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy        414 ATCAACCTCGGTCTGCAAAATGCC 437
                | |||| || || ||||||| |||
Db         26 AACAACTTCCGTTTGCAAAAAGCC 3


RESULT 10
AZ760461
LOCUS       AZ760461                  28 bp    DNA     linear   GSS 16-FEB-2001
DEFINITION  1M0554C13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0554C13 F, genomic survey sequence.
ACCESSION   AZ760461
VERSION     AZ760461.1  GI:12868327
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0554  row: C  column: 13
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 28.
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0554C13"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
```

of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 0.6%; Score 16; DB 28; Length 28;
Best Local Similarity 79.2%; Pred. No. 3.6e+07;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Qy        258 ACCCGCGACTACTACTTCGCGCTG 281
              ||| || || |||||||| | |||
Db          1 ACCTGCTACAACTACTTCCCTCTG 24
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RESULT 11
AZ323903/c
LOCUS AZ323903 29 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0045A07R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0045A07 R, genomic survey sequence.
ACCESSION AZ323903
VERSION AZ323903.1 GI:10379084
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 29)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0045 row: A column: 07
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 29.

FEATURES Location/Qualifiers
source 1. .29
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0045A07"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 0.6%; Score 16; DB 28; Length 29;
Best Local Similarity 79.2%; Pred. No. 3.7e+07;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Qy       1067 CTCCACCCGTGGTCAAGGAACTGT 1090
              || | |||||| |||| || ||||
Db         24 CTTCCCCCGTGTTCAATGACCTGT 1
```

RESULT 12
AZ658502
LOCUS AZ658502 29 bp DNA linear GSS 14-DEC-2000
DEFINITION 1M0535M12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0535M12 F, genomic survey sequence.
ACCESSION AZ658502
VERSION AZ658502.1 GI:11795564
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 29)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0535 row: M column: 12
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 29.

FEATURES Location/Qualifiers
source 1. .29
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0535M12"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 0.6%; Score 16; DB 28; Length 29;
Best Local Similarity 79.2%; Pred. No. 3.7e+07;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Qy       2224 CTGGGGAAGAGAACCTGTTCATCT 2247
              | |||| |||||| ||| | ||||
Db          5 CAGGGGCAGAGAATCTGCTGATCT 28
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RESULT 13
AZ458346
LOCUS AZ458346 30 bp DNA linear GSS 04-OCT-2000
DEFINITION 1M0262P13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0262P13 F, genomic survey sequence.
ACCESSION AZ458346
VERSION AZ458346.1 GI:10616471
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 30)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0262 row: P column: 13
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 30.
FEATURES Location/Qualifiers
source 1. .30
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0262P13"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 0.6%; Score 16; DB 28; Length 30;
Best Local Similarity 79.2%; Pred. No. 3.7e+07;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Qy       2448 GAAGCCTATGTCAAGTGTCAAGAT 2471
              |||| || ||||| |||| | |||
Db          6 GAAGTCTCTGTCAGGTGTGATGAT 29
```

RESULT 14
AU264676
LOCUS AU264676 21 bp mRNA linear EST 10-MAY-2002
DEFINITION AU264676 VS Dictyostelium discoideum cDNA clone VSD865 5', mRNA sequence.
ACCESSION AU264676
VERSION AU264676.1 GI:20523474
KEYWORDS EST.
SOURCE Dictyostelium discoideum
ORGANISM Dictyostelium discoideum
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
REFERENCE 1 (bases 1 to 21)
AUTHORS Urushihara,H., Morio,T., Saito,T., Koriki,E., Ochiai,H., Maeda,M., Takeuchi,I., Kohara,Y. and Tanaka,Y.
TITLE Population analysis of cDNAs from unicellular and multicellular stages of Dictyostelium discoideum
JOURNAL Unpublished (2002)
COMMENT Contact: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba
1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
Tel: 81-298-53-4664
Fax: 81-298-53-6614
Email: hideko@biol.tsukuba.ac.jp.
FEATURES Location/Qualifiers
source 1. .21
/organism="Dictyostelium discoideum"
/mol_type="mRNA"
/strain="AX4"
/db_xref="taxon:44689"
/clone="VSD865"
/sex="mat A"
/dev_stage="vegetative"
/clone_lib="VS"
ORIGIN

Query Match 0.6%; Score 15.8; DB 9; Length 21;
Best Local Similarity 89.5%; Pred. No. 3.4e+07;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy       2793 AATAGAGCTTAAAAATAAA 2811
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Db          2 AATAGAGATTAAAAAAAAA 20
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RESULT 15
AZ433969/c
LOCUS AZ433969 23 bp DNA linear GSS 03-OCT-2000
DEFINITION 1M0220E07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0220E07 F, genomic survey sequence.
ACCESSION AZ433969
VERSION AZ433969.1 GI:10557982
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

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            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0220  row: E  column: 07
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 23.
FEATURES              Location/Qualifiers
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                      /mol_type="genomic DNA"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="UUGC1M0220E07"
                      /sex="Male"
                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                      /clone_lib="Mouse 10kb plasmid UUGC1M library"
                      /note="Vector: PWD42nv; Purified genomic DNA from M.
                      musculus C57BL/6J (male) was obtained  from the Jackson
                      Laboratory Mouse DNA Resource
                      (http://www.jax.org/resources/documents/dnares/). The DNA
                      was hydrodynamically sheared by repeated passage through a
                      0.005 inch orifice at constant velocity. The sheared DNA
                      was blunt end-repaired with T4 DNA polymerase and T4
                      polynucleotide kinase. Adaptor oligonucleotides were
                      ligated to the blunt ends in high  molar excess. The
                      adaptored DNA was purified and size-selected for a 9.5 to
                      10.5 kb range using preparative agarose gel
                      electrophoresis. Vector DNA was prepared from a derivative
                      of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                      inducible derivative of plasmid R1. The vector was ligated
                      with adaptors complementary to the insert adaptors and
                      purified. The sheared, adaptored mouse DNA was annealed to
                      adaptored vector DNA, and transformed into
                      chemically-competent E. coli XL10-Gold (Stratagene) cells
                      and selected for ampicillin resistance."
ORIGIN

  Query Match             0.6%;  Score 15.8;  DB 28;  Length 23;
  Best Local Similarity   89.5%;  Pred. No. 3.6e+07;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1553 TCAGAATAAAACCAATGGG 1571
              |||||| |||||||||| |
Db         23 TCAGAAAAAAACCAATGTG 5


Search completed: September 15, 2004, 12:37:07
Job time : 7039 secs
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